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Q82rv0 streptomyce capture brassica ca 094ku9 brassica ca 07455 prochloroco 0911w4 pseudomonas Q8pero caenorhabdi 08744 burkholderi 09644 homo sapien Q8cgw9 mus musculu 027142 methanobact Qvrv3 drosophila Q8r3r1 mus musculu Q81zn2 musculu G81zn2 musculu 
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                 Q8u515 agrobacteri
Q8uc89 agrobacteri
Q7vsa1 bordetella
Q8ukp2 agrobacteri
Q8rtv7 uncultured
Q9zge5 heliobacill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O8tts7 methanosarc
O8s7e3 oryza sativ
O7xc01 oryza sativ
musculu
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Ovis aries (Sheep).

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vivo.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF450453; AAL47178.1; -.
SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAAB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBWN12;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
    Q8K1F8
Q8UC815
Q8UC82
Q8UKP2
Q8RUKP2
Q9AKP2
Q94FZ9
Q94FZ9
Q94FZ9
Q94FZ9
Q94FZ9
Q1530
Q1530
Q1530
Q8DERQ
Q8CGW9
Q8CW9
Q8CW
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Q9W624;
01-NOV-1999
01-NOV-1999
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Matches
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        28WN12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9jpa4 rhodocyclus
Q9kryl vibrio chol
Q7ug97 rhodopirell
Q0869 saccharomyc
Q9ryp2 deinococcus
Q8r054 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8wn12 ovis aries
                                                                                                                                                      August 12, 2004, 14:37:35; Search time 42.7151 Seconds (without alignments) 228.984 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1017041
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                          US-09-700-643A-1
167
1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRX 31
                                                                                                                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM protein - protein search, using sw model
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Q9W624
Q9LBJ6
Q7Z6Y1
Q95XJ8
Q95XJ8
Q8WW85
Q8WW85
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Q9KRY1
Q7UPG7
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Q8R054
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gápext 0.5
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sp_mammal:*
sp_mhc:*
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sp_bhage:*
sp_plant:*
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sp_bacteriap:*
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length: 2000000000
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sp_human:*
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Match Length
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Minimum DB Maximum DB

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Sequence:

Title: Perfect

Run on:

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Gaps

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34.7%; Score 58; DB 2; Length 1245; 37.5%; Pred. No. 16; 9; Indels tive 5; Mismatches 9; Indels
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56.2%;
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                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 37.55
Matches 12; Conservative
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les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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CS-ZICR1A.
Ciona savignyi.
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                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                 MEDLINE=22670508;
NCBI_TaxID=1058;
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Q95YJ8;
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0
            Carassius auratus (Goldfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii; Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodospirillum rubrum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Rhodospirillum.
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Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales,
Chromatiaceae, Thiocapsa.
                                                                                                                                                                                                                                                                                                                                                                                                                                      58.7%; Score 98; DB 13; Length 117; 56.0%; Pred. No. 2e-06; ive 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 692;
                                                                                                                                                                                      SEQUENCE FROM N.A.

TISSUE-Brain;
Satake H., Minakata H., Fujimoto M.;
'Carassius Remaide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
SEQUENCE 117 AA; 12879 WW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Last annotation update)
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Last sequence update)
Last annotation update)
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40.6%; Pred. No. 2.3;
ttive 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, BchH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 56.0 Matches 14; Conservative
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Best Local Similarity 40.6
Matches 13; Conservative
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SEQUENCE
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Q918J6;
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Phlebobranchia, Cionidae, Ciona.
NCBI_TAXID=51511;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawlor S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035608; CAB55682.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Imai K.S., Satch N., Satcu Y.;
"Ciona savignyi genes.",
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB057747; BAB68356.1; -.
InterPro; IPR007087; DRI C2H2.
Pfam: PF00096; zf-CZH2; 4.
SWART; SM00355; ZnF_CZH2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;
                                                                                                                                                                     ol-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ47997.3 (Sushi-repeat protein (SRFUL)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
1121 ABÓVALÉTŘÍRMLNPKŴÝEGMLKHGYEGVŘQI 1152
                                                                                                                                   54 AA.
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SRPUL.

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A Kaneko T. Nakamura Y., Walk C.P., Kuritz T., Sasamoto S.,
A Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
A Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M.,
Toynoplete genomic sequence of the filamentous nitrogen-fixing
T. Cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
R PIR, AH2016; AH2016.
R PIR, AH2016; Phydrolase activity; IEA.
R GO, GO:0016787; F:hydrolase activity; IEA.
R InterPro: IPR004883; M-ppestrase.
R GO, GO:00149; Metallophos; I.
R Phypothetical protein; Complete proteome.
W Hypothetical protein; Complete proteome.
SEQUENCE 303 AA; 34449 MW; 685700B2127EE987 CRC64;
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                 Strausberg R.;
Strausberg R.;
Sthmitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020733; AAH20733.1; -
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR003410; Hyalin.
InterPro; IPR004340; Hyalin.
InterPro; IPR000436; Sushi_SCR_CCP.
Ffam; PF02494; HYR; 1.
R Pfam; PF00084; sushi; 3.
SYMAT; SM00032; CCP; 3.
RPART; ENGOORS6; CYTOCHROME_P450; 1.
SEQUENCE 465 AA; 52957 MM; 3D7229487DA1B8BD CRC64;
                                                                                                                                                                                                                                                                                     34.1%; Score 57; DB 4; Length 465; llarity 56.2%; Pred. No. 8.1; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Last sequence update)
Last annotation update)
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1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein All1686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.8%; Score 56.5; DB 16;
ilarity 51.6%; Pred. No. 6.1;
Conservative 2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 HEHSYE-RIRAIDGITYLICGAGAGNRPVGR 255
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MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                            12 TPDINPAWYAGRGIRP 27
                                                                                                                                                                                                                                                                                                                                                                                                                    18 TPAVTPTWYAGSGYYP 33
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Bradyrhizobium japonicum.
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Best Local Similarity
Matches 9; Conserv
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les 16; Conserv
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Q89VA3;
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Q8YWC7
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Huang C.-H., Chen H., Peng J., Chen Y.;

"Cloning and characterization of the sushi-repeat containing protein (SRP) as a novel interaction partner of Rh type C glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                              Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Kurosawa H., Innkai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
Rakestraw K.M., Naeve C.W., Look T.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                      DB 5; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                              7; Indels
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EMBL, AF066567; AAC15765.1; -.
EMBL, AF395649; AAM73693.1; -.
EMBL, PR995649; Pelectron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR003410; Hyalin.
InterPro; IPR00436; Sushi_SCR_CCP.
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SEQUENCE 465 AA; 52971 MW; 4D752B187FF3EFB8 CRC64;
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
Metal-binding; Zinc-finger.
SEQUENCE 355 Aa; 40876 MW; E58F5DEDDB12E8AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1993 (TrEMBLrel. 55, Last annotation update)
Sushi-repeat protein (Sushi-repeat containing protein)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                         465 AA
                                                                                               34.1%; Score 57; DB 40.0%; Pred. No. 6.1; tive 7; Mismatches
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                                                                                                                                                                                                                 Created)
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QBWW87
QBWMAR-2002 (TEMBLE1 20, C)
01-MAR-2002 (TEMBLE1 20, Ls
01-MAR-2002 (TEMBLE1 20, Ls
01-MAR-2002 (TEMBLE1 20, Ls
Sushi repeat protein.
Homo sapiens (Human)
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                                                                                                 Query Match
Best Local Similarity 40.0<sup>3</sup>
Matches 12; Conservative
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Best Local Similarity
Matches 9; Conserv
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SEQUENCE FROM N.A.
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RESULT 8 Q8WW85

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Nature 406:477-483(2000).
EMBL, AE004228, AAF94657.1; -.
EMBL, AE0193, A82193, A82193, A82193, Go.; GO.0008757; F.S-adenosylmethionine-dependent methyltransf. . .; IEA.
                  Photosynthesis:
mechanisms and effects (Proceedings of the 11th international congress
on photosynthesis), pp.4:2889-2892, Kluwer Academic Publishers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIRE I TOR NISSE1 / Serotype 01;
MEDLINE=21 TOR NISSE1 / Serotype 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwirn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Raed T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                   "Dark aerobic growth conditions induce the synthesis of a high midpoint potential cytochrome c8 in the photosynthetic bacterium midpoint potential cytochrome c8 in the photosynthetic bacterium Biochemistry 38:15238-1524(1999).

Biochemistry 38:15238-1524(1999).

EMBL, AB034704; BA94057.1; -
PIR, T50904; T50904.

GO, GO:0016740; Fitransferase activity; IEA.

GO, GO:0016740; Fitransferase activity; IEA.

InterPro; IPR003672; Cobn/Mg_chltase.

Prim; PF02514; cobn-Mg_chel; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                         Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K.
Parot P., Vermeglio A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1236;
                                                                                                                                                                                                                                                                                                                                                                                    1236 AA; 134729 MW; 84051C045638520C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55997 MW; 2ABD94A2356C9E48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                   32.9%; Score 55; DB 2; 34.4%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 AHQHSMEIRTPDINPAWYAG-----RGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.6%; Score 54.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sun/nucleolar protein family protein
                                                                                                                        STRAIN=1L144;
MEDLINE=20031519; PubMed=10563807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR00051; SAM bind.
InterPro; IPR01678; Sun_Nop1/Nop2.
Pfam, PF01189; Nol1 Nop2 Sun; 1.
TIGRFAMS; TIGR00446; nop2p; 1.
PROSITE; PS01153; NoL1 NOP2 SUN; 1.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     34.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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     (eqs.);
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                         SEQUENCE FROM N.A.
                                                                       Dordrecht (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=666;
     Garab G.
                                                                                                                                                                                                                                                                                                                                                              Transferase.
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                    T "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
T Bradyrhizoblum japonicum USDAl10.";
DNA Res. 9:189-197(2002).
R REL; AP005939; BAC46409.1; -.
R GO; GO:0005310; F:NTP binding; IEA.
GO; GO:0005310; F:DNA ligase (ATP) activity; IEA.
R GO; GO:0006310; P:DNA repair; IEA.
R GO; GO:0006281; P:DNA repair; IEA.
R GO; GO:0006281; P:DNA repair; IEA.
R GO; GO:0006281; P:DNA replication; IEA.
R InterPro; IPR000977; DNA ligase.
R InterPro; IPR000977; DNA ligase.
R Pfam; PF01068; DNA ligase.
R Pfam; PF01069; DNA ligase.
R Pfam; PF01069; DNA Ligase.
R PFAM; PF04697; DNA Ligase.
R PFAM; PF0467; DNA Ligase.
R PROSITE; PS50160; DNA LIGASE A1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                  STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
KARIKO T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watenabe A., Idesawa K., Iriguchi M., Kawashina K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagashima K.V., Matsuura K., Ohyama S., Shimada K., "Primary structure and transcription of genes encoding B870 and photosynthetic reaction center apoproteins from Rubrivivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagashima K.V., Shimada K., Matsuura K., Benes of Rhodocyclus "Phylogenetic analysis of photosynthetic genes of Rhodocyclus gelatinosus: Possibility of horizontal gene transfer in purple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Bacteria, Potteobacteria, Betaproteobacteria, Burkholderiales,
Comamonadaceae, Rubrivivax.
NCBI_TaxID=28068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Igarashi N., Shimada K., Matsuura K., Nagashima K.V.;
"Photosynthetic gene cluster in purple bacterium, Rubrivivax
gelatinosus.";
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBL_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.5%; Score 56; DB 16; Length 625; Best Local Similarity 38.7%; Pred. No. 15; Matches 12; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 AA; 69415 MW; 56BED3A80A46AD42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2003 (TrEMBLrel. 24, Last annotation update)
Mg protoporphyrin methyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 HEVELIWPGLAPPYLDLFAWLEGRGEKPVNR 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [. Biol. Chem. 269:2477-2484(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94132007; PubMed=8300574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Photosyn. Res. 36:185-191(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                   SEQUENCE FROM N.A.
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us-09-700-643a-1.rspt

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Search completed: August 12, 2004, 14:48:58 Job time: 44.7151 secs
                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       radiodurans R1.";
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                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C.M.;
                                                                                                                                                                                                                                                     Q9RYP2
Q9RYP2;
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               ï
               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97298311; PubMed=9153759;
Mauniaux J.C., Poirey R.;
Jauniaux J.C., Poirey R.;
Sequencing analysis of a 36.8 kb fragment of yeast chromosome XV reveals 26 open reading frames including SEC63, CDC31, SUG2, GCD1, Yeast 13:483-487(1997)

BMBL, PATT, PAC1 and VPH1.";
BMBL, Z75161; CAA99475.1; -..
SCD: SCO05779; NATS.
GO: GO:0005737; C:cytoplasm; IC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
0
               1;
                                                                                                                                                                                                                                                               Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.3%; Score 54; DB 16; Length 1120; 64.3%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
EMBL, BX224145; CAD75095.1; -
Hypotherical protein; Complete proteome.
SEQUENCE 1120 AA, 123221 MW, 67C757B73421BF9B CRC64;
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 05, Last annotation update)
Chromosome XV reading frame ORF YOR253W.
NATS OR ARD2 OR YOR253W.
                                                                                                                                                                                              Last sequence update)
Last annotation update)
               12;
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                                                                                                                                                   PRT; 1120 AA
                                                                 | : ||:|: | : | | : | 435 SSASHSVELDTTQAR-EWFMGRDVRPEGQ 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
Best Local Similarity 36.7%; Pred. No. 20;
Matches 11; Conservative 6; Mismatches
                                              1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22735913; PubMed=12835416;
                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, Hypothetical protein.
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202 EISPAWWAKMGIRP 215
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Best Local Similarity 64.3
Matches 9; Conservative
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                                                                                                                     RESULT 13
Q7UPG7
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MEDLINE=20036996; PubMed=10567266;
White O., Elsen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D.,
White D.G., Gavinn M.L., Nelson W.C., Richardson D.L.,
Moffet K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann K.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                              Gaps
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0
                                                                                                                                                      Length 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.7%; Score 53; DB 16; Length 376; 40.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcace
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                                                                                                                                                                                                              Indels
InterPro; IPR000182; CytC_heme_BS.
InterPro; IPR000182; GGNBacetyl_trans.
Pfam, PF00583; Acetyltransf; 1.
PROSTIE; PS00190; CYTOCHROME_C; 1.
SEQUENCE 176 AA; 19727 MW; 4F09DC597A690BA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 AA; 39845 MW; 7AB7FF32F8C45651 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                   32.0%; Score 53.5; DB 3; ilarity 31.2%; Pred. No. 9.3; Conservative 5; Mismatches 14;
                                                                                                                                                                                                                                                                                                                  120 SECHÖHNVFVYLPAVDDLTKOWFIAHGFEOVG 151
                                                                                                                                                                                                                                                                 1 SRAHQHSMEIRTP---DINPAWYAGRGIRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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EMBL; AE001863; AAF12376.1; -.
PIR; C75580; C75580.
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Best Local Similarity 40.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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5,1.6 Compugen Ltd. GenCore version Copyright (c) 1993 - 2004

OM protein - protein search, using sw model

August 12, 2004, 14:37:36; Search time 13.6977 Seconds (without alignments) 217.697 Million cell updates/sec Run on:

US-09-700-643A-1 167

1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRX Perfect score: Sequence:

31

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 78: * 2: pir1: * 2: pir2: * 3: pir3: * Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	prolactin-releasin	hypothetical prote	Mg protoporphyrin	Sun/nycleolar prot	ical p	eami	hypothetical prote	transcription regu	Fok family protein	/hypothetical prote	probable magnesium	_	/ hypothetical_prote	Conserved hypothet	probable unr prote	hypothetical prote	ρ	a]	_	аJ	ដ	cal	probable regulator	В	hypothetical prote	al	hetical prot	ein	histi
SUMMAKLES	DI	JC7607	AH2016	5090		867150	C75580			B97672	9	146	337	107	900	121	317	AB2664	744	795	695	681	754	0	329	7056	164	3909	3817	8755
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oh	Query	1 4	33.8	ď.	ď.	•	31.7	31.1		31.1	ä	ч	ö	ö	ö	ö	φ.	29.6	φ.	φ.	ď.	φ.	ο,	œ.	ω.	28.7	ω ω	28.7	ω,	28.7
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	Result No.	7	2	m	4	2	9	7	œ	σ	10	11	12	13	14			17		19	20	21	22	23	24	25	26	27	28	29

protoporphyrin IX	magnesium chelatas	biotin sulfoxide r	11-beta-hydroxyste	exo-alpha-sialidas	probable aldC prot	sensory transducti	hypothetical prote	N-acetylglutamate	conserved hypothet						
T07958	AE2351	875000	837310	S64721	S71288 ·	T01789	T07126	AD0982	I46535	JC7588	D70885	F69099	T33759	D84012	AB0729
,	~	~	N	N	7	~	~	(7)	0	~	~	~	0	~	7
772	1328	1331	1379	1380	1381	1382	1383	777	406	418	455	785	1084	345	479
28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.4	28.1	28.1	28.1	28.1	28.1	27.8	27.8
48	48	48	48		48	4.8	48	47.5	47	47	47	47	47	46.5	46.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

RESULT 1

prolactin-releasing peptide - rat
C;Species; Raftus norvegicus (Norway rat)
C;Species; Raftus norvegicus (Norway rat)
C;Species; Raftus norvegicus
C;Species; Raftus norvegicus
C;Species; Raftus norvegicus
C;Species; Saftus norvegicus
C;Species; Saftus norvegicus
R;Yanada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T.
B;Species; M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T.
B;Species; M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T.
B;Species: Isolation and characterization of the rat prolactin-releasing peptide gene: Mul
A;Contents: Spleen
A;Contents: Spleen
A;Contents: Spleen
A;Contents: Spleen
A;Contents: DNA
A;Contents: 1-83 - YAM'
A;Contents: 1-83 - YAM'
A;Contents: 1-83 - YAM'
A;Contents: 1-83 - YAM'
A;Contents: This peptide induces arachidonic acid metabolite release from rat anterior pi
C;Genetics:
A;Gene: PRR
A;Introns: 33/1

Gaps .; 0 Length 83; Indels 2; Score 157; DB 2; Pred. No. 6e-16; 0; Mismatches 2 , 94.0%; 93.3%; Conservative Query Match Best Local Similarity Matches 28; Conserv

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hypothetical protein all1686 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. etrain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 24-Nov-2003
C;Accession: AH2016

A; Residues: 1, 2003 (KUL>) A; Residues 1.030 (KUL>) A; Residues: 1.030 (KUL>) A; Experimental source: strain PCC 7120

C,Genetics: A,Gene: all1686

C; Superfamily: tartrate-resistant acid phosphatase

., 8 5

Score 56.5; D Pred. No. 1.5; 2; Mismatches

Query Match
Best Local Similarity 51.6%;
Matches 16; Conservative

226 HEHSYE-RTRAIDGTTYLTCGAGAGNRPVGR 255

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4 HQHSMEIRTPDINPAWY ---- AGRGIRPVGR 30

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hypothetical protein AGR_L 109 [imported] - Agrobacterium tumefaciens (strain C58, Cereor C; Species: Agrobacterium tumefaciens
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C; Accession: A98137
R; Goodner, B.; Hinke, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
               C)Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C)Accession: S67150
C)Accession: S67150
E)Aduniaux, J.C.; Poirey, R.
Submitted to the Protein Sequence Database, July 1996
A;Reference number: S67143
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-176 cJAU>
A;Residues: 1-176 cJAU>
A;Residues: 1-176 cJAU>
A;Residues: SMBL:275161; NID:g1420572; PID:e252411; PID:g1420573; GSPDB:GN00015;
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CjAccession: C75580
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F. Mishite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Ma.; Shen, M.; Vamathevan, J.U.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mal, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum: A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A99137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12376.1; PID:g6460677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenine deaminase-related protein - Deinococcus radiodurans (strain R1)
C,Species: Deinococcus radiodurans
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECHQHNVFVYLPAVDDLTKQWFIAHGFEQVG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SRAHQHSMEIRTP---DINPAWYAGRGIRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53.5;
Pred. No. 2.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.0%;
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40.0%;
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A;Map position: 15R
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Best Local Similarity 31.29
Matches 10, Conservative
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Best Local Similarity 40.0
Matches 12; Conservative
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A; Residues: 1-73 < KUR>
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                                                                                                                                                                                                                                                                                                                                                    A; Gene: MIPS:YOR253w
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                                                                                                                                                                                                                                                                                                                     Mg protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus C; Species: Rubrivivax gelatinosus C; Species: Rubrivivax gelatinosus C; Species: 21-Uul-2000 #sequence_revision 21-Uul-2000 #text_change 02-Sep-2000 C; Accession: T50904 K: T50904 K: V: Igarashi, N: Harada, J: Nagashima, S: Matsuura, K: Shimada, K: submitted to the EMBL Data Library, November 1999 A; Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
Cémentics:
A;Gene: VO1502
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A82103
Sun/nucleolar protein family protein VC1502 [imported] - Vibrio cholerae (strain N16961
Sun/nucleolar protein family protein VC1502 [imported] - Vibrio cholerae (strain N16961
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: A82193
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ernolaeva, M.D.; Vanathevan, J.; Bass, S.; Qin, H.; Draggi, I.; Sellers, H.
Nature 4.06, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUD: 20406833; PMID: 10952301
A;Ccession: A82193
A;Accession: A82193
A;Anlecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C)Genetics:
A;Gene: bchH
C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
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Length 303;
                                                           Indels
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ch 32.9%; Score 55; DB 2; Similarity 34.4%; Pred. No. 11; 11; Conservative 6; Mismatches 5

Local Similarity

Best Loc Matches

à

A,Status: preliminary, translated from GB/EMBL/DDBJA,Molecule type: DNA A;Residues: 1-1236 <NAG>
A;Cross-references: EMBL:AB034704; PIDN:BAA94057.1
A;Experimental source: strain IL144

A; Reference number: Z25270

A; Accession: T50904

3 AHQHSMEIRTPDINPAWYAG-----RGIRPV 28

867150 hypothetical protein YOR253w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein 05315

435 SSSASHSVELDTTQAR-EWFMGRDVRPEGQ 463

1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30

32.6%; Score 54.5; DB 2; 36.7%; Pred. No. 5;

Query Match 32.6 Best Local Similarity 36.7 Matches 11; Conservative

A, Residues: 1-503 <HEI>

12;

6; Mismatches

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hypothetical protein ugpB [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pl C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 (Accession: AH3166 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Frace, P.; Romero, P.; Zhang, S.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2117-2333, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.J.; Br
K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable magnesium chelatase (EC 4.99.1.-) chain H BchH - Heliobacillus mobilis C;Species: Heliobacillus mobilis C;Species: Heliobacillus mobilis C;Species: Heliobacillus mobilis C;Species: Heliobacillus mobilis C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000 C;Accession: T31462 Hs. K:Xiong, U.; Inoue, K.; Bauer, C.E. Proc. Natl. Acad. Sci. U.S.A. 95, 14851-14856, 1998 A;Title: Tracking molecular evolution of photosynthesis by characterization of a major k A;Reference number: 221036; MUID:99061957; PMID:9843979 A;Accession: T31462 A;Accession: T31462 A;Accession: T31462 A;Amolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: bchH
Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                        Ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Acession: AH3166

A;Status: preliminary

A;Nolecule type: DNA

A;Residues: 1-419 < KUR>

A;Cross-references: GB:AE008687; PIDN:AA145750.1; PID:g1743483; GSPDB:GN00188

A;Experimental source: strain C58 (Dupont)
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A;Cross-references: EMBL:AF080002; NID:g3820536; PID:g3820560; PIDN:AAC84033.1
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Pred. No. 9.5;
5; Mismatches
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Pred. No. 32;
3; Mismatches
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     AHLHRQEMISEDIIAAWQAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 SPEANATWFAGTGYLPINK 341
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ilarity 36.8%;
Conservative 5
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ilarity 38.5%;
Conservative
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Best Local Similarity
Matches 10; Conserva
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Best Local Similarity
Matches 7; Conserv
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C, Genetics:
A, Gene: bchh
C, Superfamily: Rhod
C, Keywords: lyase
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A;Gene: ugpB
A;Genome: plasmid
     196
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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A; Reference number: A97359; MUD:21608551; PMID:11743194
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-308 < KUR>
A; Residues: 1-308 < KUR>
A; Gene: AGE
A; Gene: Cs:
A; Gene: AGE
A; Gene: AGE
C; Superfamily: conserved hypothetical protein HI0182; glucose kinase homology
                                                                                                                                                                                                                                                                                                                                                                               transcription regulator, ROK family Atu2609 [imported] - Agrobacterium tumefaciens (stra
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH2896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rok family protein VC1532 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) C; Species: Agrobacterium tumefaciens C; Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C; Accession: B97672 C; Accession: B97672 R; Godder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm.
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A, Accession: AH2886
A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Coss. references: GB. AE008688; PIDN: AAL43590.1; PID:g17741107; GSPDB:GN00186
A, Experimental source: strain CS8 (Dupont)
A, Coss. references: GB. AE008688; PIDN: AAL43590.1; PID:g17741107; GSPDB:GN00186
A, Experimental source: strain CS8 (Dupont)
A, Gene: Atu3609
A, Map position: dircular chromosome
C, Superfamily: conserved hypothetical protein H10182; glucose kinase homology
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                                                                                  DB 2; Length 73;
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50.0%; Pred. No. 6.9;
iive 2; Mismatches
                                                                          Query Match 31.1%; Score 52; DB Best Local Similarity 47.6%; Pred. No. 1.5; Matches 10; Conservative 3; Mismatches
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A, Gene: AGR L 109
A, Map position: linear chromosome
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Matches 10; Conserv
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Search completed: August 12, 2004, 14:50:24 Job time : 14.6977 secs
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                                                                                                 A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor, A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference preliminary
A;Residues: preliminary
A;Residues: 1-664 <STO>
A;Residues: 1-664 <STO>
A;Residues: 1-664 <STO>
A;Residues: 1-664 <STO>
A;Gross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN001
C;Genetics:
A;Gross-references: Strain PAO1
C;Genetics: A;Genetics: A;Ge
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A, Reference number: A69000; MUID:98037514; PMID:9371463
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A;Cross-references: EMBL:Z50873; PIDN:CAA90762.1; GSPDB:GN00028; CESP:F19H6.1
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A;Experimental source: clone F19H6
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T21075; T21124
R;McMurray, A.
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A;Introns: 55/3; 85/2; 113/3; 150/1; 192/3; 266/2
C;Superfamily: kinase-related transforming protein; protein kinase homology
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Pred. No. 19;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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Best Local Similarity 44.8%; Pred. No. 9.2;
Matches 13; Conservative 2; Mismatches 13
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submitted to the EMBL Data Library, November 1995
A,Reference number: Z19376
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A;Reference number: 219368
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Best Local Similarity 55.6%;
Matches 10; Conservative
.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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A,Gene: CESP:F19H6.1
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A;Residues: 1-430 <MTH>
A;Cross-references: GB:AE000877; GB:AE000666; NID:g2622157; PIDN:AAB85559.1; PID:g2622161
A;Experimental source: strain Delta H
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Cippecies: Rattus norvegicus (Norway rat)
Cippecies: Rattus norvegicus (Norway rat)
Cipate: 21.Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
Cipacession: S11210
Rijeffers, M.; Paciucai, R.; Pellicer, A.
Nucleic Acids Res. 18, 4891-4899, 1990
A;Title: Characterization of unr; a gene closely linked to N-ras.
A;Reference number: S11210; MUID:90370473; PMID:2204029
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A,Residues: 1-796 «JEF»
A,Cross-references: BMB:X52311; NID:g57454; PIDN:CAA36549.1; PID:g57455
C,Keywords: DNA binding
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             A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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Pred. No. 14;
0; Mismatches 4; Indels
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Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.5%; Score 51; DB Best Local Similarity 43.5%; Pred. No. 27; Matches 10; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                  30.5%;
69.2%;
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Query Match
Best Local Similarity 69.2.
Best Local Similarity 69.2.
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A; Accession: B69009
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August 12, 2004, 14:37:35 ; Search time 8.11047 Seconds (without alignments) 199.024 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-700-643A-1 167 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRX 31

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 Total number of hits satisfying chosen parameters:

141681 segs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		P81264 bos taurus	m		bos t	Q9uq49 homo sapien									P51976 oryctolagus		Q8q001 methanosarc	-				-		Q9fbm3 streptomyce			_						റ	
SUMMARIES	ID	PRRP BOVIN	PRRP_RAT	PRRP_HUMAN	NER3 BOVIN	NER3 HUMAN	EX7L COREF	EX7L_CORGL	UNR RAT	Y587 PASMU	6PGL_SYNY3	SAMB_SALTY	T2D3_HUMAN	XERC_VIBVU	DHI2 RABIT	NER3 RAT	TRB2 METMA	M4K6 MOUSE	ARGC_BACHD	AVP3 ARATH	DAPF CORGL	Y762_METUA	YS76_METJA	EX7L_STRCO	YCGB ECOLI	UNR_HUMAN	TGM1 RABIT	TRA2 DROVI			SUV1 ARATH	LIPM NEIMB	HIS8 HALN1	NER3 MOTISE
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Gaps

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Query Match
99.4%; Score 166; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 30; Conservative 0; Mismatches 0; Indels

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P39743 saccharomyc P22735 homo sapien P23606 rattus norv C26543 methanobact Q91477 arabidopsis P72052 mycobacteri P72156 pseudomonas Q9468 homo sapien P20099 escherichia P58302 thermoplasm Q9ryd4 deinococcus Q47499 erwinia chr	nnce update) attion update) attion update) attion update) attion update) attion update) artinuupdate) artinuupdate) artinuupdate) aniata, Vertebrata, Euteleostomi; yla; Ruminantia; Pecora; Bovoidea; (OF 23-52.); Kawamata Y., Hosoya M., Fukusumi S., Rawamata Y., Askiguchi M., atsumoto H., Sekiguchi M., n the brain."; n	108 CRC64;
R167 YEAST TGMI_HUMAN TGMI_RAT UVRA_METTH ACAC_ARATH X116 MYCTU ATZA_PSESD LMBT_HUMAN BISC_ECOLI RASO_THEVO NPD_DEIRA		οŽ.
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335 335 335 335 337 444 445 444 444 444 444 444 444 444 44	RESULT 1 PRRP BOVIN AC PRAY-2000 (Rel. 39, C DT 30-MAY-2000 (Rel. 39, L DE PARP-2000 (Rel. 39, L DE PARP-2000 (Rel. 39, L DE PARY-2000 (Rel. 39, R) DE PARY-2000 (Rel. 30, R) DE PARY-2000 (Rel. 3	SEQUENCE 9
	PRESENT PROCESS OF STREET PROC	O'S

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PRRP HUMAN
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SEQUENCE
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                              SEQUENCE
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PRRP_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afterement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Sprague-Dawley; TISSUE-Hypothalamus; Anderson S.T., Xokay I.C., Lang T., Grattan D.R., Curlewis J.D.; Anderson S.T., Xokay I.C., Lang T., Grattan D.R., Curlewis J.D.; "Quantitation of prolactin-releasing peptide (PPRP) mRNA expression in specific brain regions during the rat oestrous cycle and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-53 PROVIDE AMIDE GROUP).
TPDINPAWYTGRGIRPVGREGRRATPRDVTGLGGLSCLPL
DGRTKFSQRG -> SECLTYGKQPLISFHPPTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                       Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.; "A prolactin-releasing peptide in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY.
MEDLINE=99426652; PubMed=10498338;
Fuji R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sumino Y., Fujino M.; "Tissue distribution of prolactin-releasing peptide (PrRP) and its
RESULT 2
PRRP RAT
1D FRRP RAT
AC PR1278; Q8K3YC;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-PED-2003 (Rel. 41, Last annotation update)
DT 28-PED-2003 (Rel. 41, Last annotation update)
DF Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing DE hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isold=P81278-2; Sequence=VSP_004370;
TISSUE SPECIFICITY: Widely expressed, with highest levels in
medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AFDZIJOU; AFDZIGOTO PRINCIPLE OF BASIC residues; Alternative splicing.

Alternative splicing.

SIGNAL 1 21 BY SIMILARITY.

PEPTIDE 22 52 PROLACTIN-RELEASING PEPTIDE PRRP31 PEPTIDE 33 52 PROLACTIN-RELEASING PEPTIDE PRRP20 PROPEP 57 83 AMIDATION (G-53 PROVIDE AMIDE GROUVARRELIC 33 83 AMIDATION (G-53 PROVIDE AMIDE GROUVARRELIC 33 83 AMIDATION (G-54 PROVIDE AMIDE GROUVARRELIC 33 83 AMIDATION (G-54 PROVIDE AMIDE GROUVARRELIC 35 SECLIYGROPHESQ
                                                                                                                                                                                                                                                                                                                                                                                                                                    lactation.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P81278-1; Sequence=Displayed
                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=98268781; PubMed=9607765;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB015418; BAA29026.1; -. EMBL; AF521930; AAM82154.1; -.
                                                                                                                                releasing peptide PrRP20].
                                                                                                                                                                                                                                                                                                                                   Nature 393:272-276(1998)
                                                                                                                                                                                                  NCBI_TaxID=10116;
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FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.

TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99426652; PubMed=10499338; Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sumino Y., Fujimo M.; Tujimo M.; Tissue distribution of prolactin-releasing peptide (PrRP) and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fukusumi S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          John V. 2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing
hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PROLACTIN-RELEASING PEPTIDE PRRP20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 87;
                                                                                                   Score 157; DB 1; Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 152; DB 1; Length 87
Pred. No. 1.7e-15;
1; Mismatches 2; Indels
                                                                                                                                                        2; Indels
isoform 2).
/FTId=VSP_004370.
DOC75A264EEE4F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229A2F3F50CF981B CRC64;
                                                                                                                               3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                87 AA
                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                 51
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                                                                                                                                                                                                            SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                              AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:peptide hormone; TAS.
                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98268781; PubMed=9607765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB015419; BAA29027.1; -.
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9639 MW;
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                                                                                                   Query Match
Best Local Similarity 93.3%;
Matches 28, Conservative
                                                       9215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 releasing peptide PrRP20]
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                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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les 27; Conserv
                                                       83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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34
58
53
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
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SRAHQHSMEIRTPDINPAWYAGRGIRPVGR

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                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
38-FEB-2003 (Rel. 41, Last annotation update)
(N-acetyl-alpha-neuraminidase 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoconjugates.

GTALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and characterization of a plasma membrane-associated sialidase specific for gangliosides.";
J. Biol. Chem. 274:5004-5011 (1999).
-:- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                                                                                                                                                                                                            ω
.
                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidea, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                        MEDLINE=99143165; PubMed=9988745;
Miyagi I., Wada T., Iwamatsu A., Hata K., Yoshikawa Y., Tokuyama
Sawada M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SÜBCELLULAR LOCATION: Membrane-associated (By similarity)
-!- TISSUE SPECIFICITY: Expressed in brain.
-!- SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
-!- SIMILARITY: Contains 3 BNR repeats.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.5%; Score 61; DB 1; Length 428; 40.7%; Pred. No. 0.21;
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BNR 2.
BNR 3.
FRIP MOTIF.
By similarity.
Potential.
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By similarity.
Potential.
                                                                                         428 AA.
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InterPro. 1 PR0020860; GH_BNR.
Pfam, PF02012; BNR, 3.
Hydrolase, Glycosidase, Membrane, Repeat.
Potential.
Potential.
Potential.
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                                                                                         PRT;
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                                                                                     STANDARD;
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265
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es 11; Conserv
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254
224
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28-FEB-2003
28-FEB-2003
Sialidase 3
                                                                                       NER3 BOVIN
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. 0

Gaps

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Indels

10;

Pred. No. 0.21; 6; Mismatches

Conservative

Best Loc Matches

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                                                                                                                                NER3 HUMAN
O9UQ49; QSNQE1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
-1144se 3 (EC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUES.Skeletal muscle;

TISSUES.Skeletal muscle;

PUDMed=10861246;

MONTI E., Bassi M.T., Papini N., Riboni M., Manzoni M., Venerando B., Croci G., Preti A., Ballabio A., Tettamanti G., Borsani G., "dentification and expression of NBU3, a novel human sialidase associated to the plasma membrane.";

Blochem. J. 349:343-351(200).

-i. FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wada I., Yoshikawa Y., Tokuyama S., Kuwabara M., Akita H., Miyagi T., "Cloning, expression, and chromosomal mapping of a human ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycoconjugates.
CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-, oligosaccharides, glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SÜBCELLULAR LOCATION: Membrane-associated.
-:- TISSUE SPECIFICITY: Highly expressed in skeletal muscle, testis, adrenal gland and thymus, followed by pancreas, liver, heart and thymus. Weakly expressed in kidney, placenta, brain and lung.
-:- MISCELLANDENCHS: Optimum pH is 3.8.
-:- SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Min; 604617; -. Golo05887; C:integral to plasma membrane; TAS. GO; GO:0003824; F:catalytic activity; TAS. GO; GO:000689; P:ganglioside catabolism; TAS. InterPro; IPR002860; GH BNR. S. Pfam; PF02012; BNR; 3. Pfam; PF02012; BNR; 3. Rydrolase; Glycosidase; Membrane; Repeat. T REPEAT 129 140 BNR 1. T REPEAT 203 214 BNR 2. T REPEAT 203 214 BNR 3. T SITE 254 265 BNR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 261:21-27(1999)
                             195 RARPHSLMIYSDDLGATWHHGRLIKPM 221
2 RAHOHSMEIRTPDINPAWYAGRGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB008185; BAA82611.1; -.
EMBL; Y18563; CAE96131.1; ALT_INIT.
Genew; HGNC:7760; NEU3.
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99335353; PubMed=10405317;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sialidase.
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4

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UNR_RAT STANDARD; PRT; 798 AA. P18395.
01-807-1990 (Rel. 16, Last sequence update)
116-0CT-2001 (Rel. 40, Last annotation update)
UNR protein.
57.1%; Pred. No. 4.3; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP, MF_00378, -; 1.
Interpro; IPR003753; Exonuc_VII_L.
Interpro; IPR008994; Nucleic_acid_OB.
                                                                                     90 PAFYAGRGSFSLWVTDIRPVG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 PAFYAGRGTFSLWVTDIRPVG 114
                                                           -----IRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 PAWYAGRG-----IRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP005277; BAB98418.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02601; Exonuc VII L;
TIGRFAMS; TIGR00237; xseA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 57.1;
Matches 12; Conservative
                       12; Conservative
                                                                                                                                                                                                    STANDARD;
    Best Local Similarity
                                                             17 PAWYAGRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawa S.;
                                                                                                                                                                                                      CORGL
                                                                                                                                                                                                        EX7L CON
QBNRM3;
                                                                                                                                                                                 EX7L_CORGL
AC AC BE FEB DT 28-FEB DT
                       Matches
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                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 13:1572-1579(2003).
-1- FUNCTION: Bidirectionally degrades single-stranded DNA into large
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity). CATALYITC ACTIVITY: Exonucleolytic cleavage in either 5' to 3' or 3' to 5'-direction to yield nucleoside 5'-phosphates. SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-0cT-2003 (Rel. 42, Created)
10-0cT-2003 (Rel. 42, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 413;
                                                                                                                                                                                                                           Score 56; DB 1; Length 428; Pred. No. 1.2;
                                                                                                                                                                                                                                                                    11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Arvosa...
HAMAP, MF_00078; -: 1.
IINENTRO, IPR003753; Exonuc_VII_L.
IINENTRO, IPR008994; Nucleic_acid_OB.
Pfam, PF02601; Exonuc_VII_L; 1.
IIGR0237; XseA, 1.
IIGR0237; XseA, 1.
IYGRAFAMS; TIGR00237; XseA, 1.
IYGRAFAMS; TIGR00237; XseA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the xseA family.
                                                                                                                                                                                   35D1DD9359A78C98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                                   Potential.
Potential.
By similarity.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 AA
        similarity.
                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                    195 KTRPHSLMIYSDDLGVTWHHGRLIRPM 221
                                                                                                                                                                                                                                                                                                             2 RAHQHSMEIRTPDINPAWYAGRGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52;
      By similar
Potential.
Potential.
Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Exonuclease VII large subunit)
                                                                                                                                                                                       48252 MW;
                                                                                                                                                                                                                              33.5%;
37.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium efficiens.
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
        25
45
50
87
225
340
340
                                                                                                                                                                                                                                             Local Similaritý
nes 10; Conserv
                                                                                                                                                                                         428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=152794;
        25
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87
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3370
387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gojobori T.;
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Q8FQF1;
    ACT SITE
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                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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        FTTFFFF
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ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.", Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonuclectides, which are then degraded further into small acid-soluble oligonuclectides (By similarity).
-!- CATALVITIC ACTIVITY: Excuncileolytic cleavage in either 5' to 3'- or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
-!- SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Gaps
8
                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 4), Last sequence update)
28-FEB-2003 (Rel. 4), Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
(Exonuclease VII large subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baccerla; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.1%; Score 52; DB 1; Length 417; 57.1%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
Indels
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SEQUENCE 417 AA, 45582 MW, B32CD9286C173C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1. SUBCELLUTÂR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum (Brevibacterium flavum).
ö
                                                                                                                                                                                                                                                                                                                          417 AA.
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    -!- SIMILARITY: Belongs to the fructosamine kinase family.

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                                                                                                                                                                                                                                                                                     SYNY3
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                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Pm70;
MEDLINE=21145866; PubNed=11248100;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                 Jeffers M., Paciucci R., Pellicer A., "Characterization of unr; a gene closely linked to N-ras."; Nucleic Acids Res. 184891-4899(1990).
-!- FUNCTION: RNA-binding procein (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.5%; Score 51; DB 1; Length 798; 43.5%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                             CSD 1.
CSD 3.
CSD 3.
CSD 4. (INCOMPLETE).
CSD 5.
CSD 6.
CSD 6.
CSD 7.
CSD 7.
CSD 7.
CSD 9.
CSD 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein PMOS87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                           HSSP, P15277; 1MJC.
InterPro; IRR002059; Cold shock.
InterPro; IRR002059; Cold shock.
InterPro; IRR002059; Nucleic_acid_OB.
Pfam; PP00313; CSD; 7.
ProDom; PD000621; Cold_shock; 1.
SMART; SM00357; CSP; 5.
PROSITE; PS00352; COLD_SHOCK; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   583 HSVNGITEEANPTIYSGKVIRPL 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 HSMEIRTPDINPAWYAGRGIRPV 28
                                                                       MEDLINE=90370473; PubMed=2204029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           88894 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                   245
337
410
507
                                                                                                                                                                                                                                                                                                                                                                                                           579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                        798 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                       349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Matt.
The Local Simit
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phospho-D-gluconate.
PATHWAY: Pentose phosphate pathway; second step.
SIMILARITY: Belongs to the glucosamine/galactosamine-6-phosphate isomerase family. 6-phosphogluconolactonase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Hydrolysis of 6-phosphogluconolactone to 6-phosphogluconate.
-!- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE OF 1-19.
MEDLINE=97443974; PubMed=9298645;
SAZUKA T., Ohara O.;
"Towards a protecome project of cyanobacterium Synechocystis sp.
"Towards a protecome project of cyanobacterium Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                           EMBL; AE006094; AAK02671.1; -.
InterPro; IPR005581; Fructosamin kin.
Pfam; PF03881; Fructosamin kin; I.
Hypothetical protein; Transferase; Kinase; Complete proteome.
SEQUENCE 288 AA; 33778 MW; F4D2F6C26014D940 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last Sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
PGL OR DEVB OR SIL149.
Synechocystis sp. (strain PCC 6803).
Bacteria, Cyanobacteria, Chrococcales, Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.9%; Score 50; DB 1
37.5%; Pred. No. 5.9;
iive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 QHSMEIRTPDINPAWYAGRGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 KHKEKIHTGEMHEAWIIDDGIQPV 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes.";
Electrophoresis 18:1252-1258(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 37.55,
Conservative
Conservative
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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0
                                                                                                                  Length 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nohmi T., Hakura A., Nakai Y., Watanabe M., Murayama S.Y.,
                                                                                                                                             Indels
                                                                                            239 AA; 26351 MW; 9C64A0A342325917 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FF8C47476CC58A2B CRC64;
                                                                                                                                             6
                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                       01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                   Score 48.5; D
Pred. No. 8.1;
5; Mismatches
                                                                                                                                                                                               198 OHALGEIFAPEADPOOYPARFIOPOG 223
                                                                                                                                                                      5 QHSM-EIRTPDINPAWYAGRGIRPVG 29
EMBL; D90916; BAA18726.1; ALT INIT.
InterPro; IPR006148; Gluc_gal_isom.
InterPro; IPR005900; Phosphogluconlac.
Pfam; PF01182; Glucosamine iso; 1.
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Plasmid; SOS mutagenesis; DNA repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=LT2;
MEDLINE=91123176; PubMed=1991707;
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IPR001126; UMUC_like.
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                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47727 MW;
                                                                 Hydrolase, Complete proteome.
INIT MET 0 0 SEQUENCE 239 AA; 26351 MW;
                                                                                                                             11; Conservative
                                                                                                                      29.08;
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                                                     TIGRFAMS; TIGRO1198; pgl;
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SAMB_SALTY STANDARD;
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                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SAMB.
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REDIENCE FROM N.A.

REDIENCE FROM N.A.

REDIENCE 1638749; PubMed=11780052;

REDIENCE 21638749; PubMed=1178040; Redience 217874;

REDIENCE 21638749; PubMed=1178040; Redience 217874;

REDIENCE 21638749; PubMed=1178040; Redience 217874;

REDIENCE 21638749; PubMed=117874;

REDIENCE 21638749; PubMed=117874;

REDIENCE 21638749; REDIENCE 2164874;

REDIENCE 21638749;

REDIENCE 21638749; REDIENCE 2163874;

REDIENCE 21638744; REDIENCE 2163874;

REDIENCE 21638744; REDIENCE 2163874;

REDIENCE 21638744; REDIENCE 2163874;

REDIENCE 21638744; REDIENCE 2163874;

REDIENCE 21638744;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complex
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MEDLINE=97098442; PubMed=8942982;
Tanese N., Saluja D., Vassallo M.F., Chen J.-L., Admon A.;
"Molecular cloning and analysis of two subunits of the human TFIID complex: hTAFIII30 and hTAFII100.";
Proc. Natl. Acad. Sci. U.S.A. 93:13611-13616(1996).
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MEDLINE-20063193; PubMed-10594036;
Gangloff Y.-G., Werten S., Romier C., Carre L., Poch O., Moras D.,
                                                                                                                                                                                                                                                  Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
T123 HUMAN STANDARD, PRI; 1083 AA.
C00268; Q99721; Q9BR40; Q9BK42;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 37, Last sequence reliance)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2019 (Rel. 43) (Astinitiation factor TFIID 135 kDa subunit (TAFII-135)
(TAFIII35) (TAFII-130).
TAF4 OR TAF4A OR TAF2C1 OR TAF2C OR TAFII135 OR TAFII130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DENTIFICATION IN THE TFTC-HAT COMPLEX WITH TAFSL; TAF6L; TADA3L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 870-918 IN COMPLEX WITH
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MEDLINE=99303588; PubMed=10373431;
Brand M.; Yamamoto K.; Staub A.; Tora L.;
"Identification of TATA-binding protein-free TAFII-containing subunits suggests a role in nucleosome acetylation and signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 274:18285-18289(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes Dev. 11:1381-1395(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 414:865-871(2001).
                                                                                                                                                                                                                                    (Human)
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mammalian cells."
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                               10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Tyrosine recombinase xerC.
                                                                                                                                                                                                                                               Vibrionaceae, Vibrio.
NCBI_TaxID=672;
                                                                                                                                                                                 Vibrio vulnificus.
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                                                                                pairs.";
Mol. Cell. Biol. 20:340-351(2000).
Mol. Cell. Biol. 20:340-351(2000).
Mol. Cell. Biol. 20:340-351(2000).
Mol. Cell. Biol. 20:340-351 of the mediating promoter responses to various plays a central role in mediating promoter responses to various activators and repressors. Potentiates transcriptional activation by the AF-2S of the retinoic acid, vitamin D3 and thyroid hormone.
-!- SUBUNIT: TFIID is composed of TATA binding procein (TBP) and a number of TBP-associated factors (TAFS). Component of the TFTC-HAT complex, at least composed of TAFE, TAPEL, TADA3L, SUPT3H/SPT3, TAFZ/TAFIIISO, TAF4/TAFIII3S, TAF5/TAFIIIOO, GCNSL2/GCNS, TAFIO
Davidson I.; "The number of TAF(II) 135 and TAF(II) 20 and the yeast "The numan TFIID components TAF(II) 68 heterodimerize to form histone-like SAGA components ADA1 and TAF(II) 68 heterodimerize to form histone-like
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REMBL; AL137077; CACGG006.1; ...

REMBL; AL137077; CACGG006.1; ...

REMBL; AL130911; CAC22312.2; ...

REMBL; AL130911; TAPF, ...

REMBL; AL130911; TAPF, ...

REMBL; AL130911; TAPF, ...

REMBL; AL130, AL120, A
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                                                                                                                                                                                                                                                                                                                                                                                  and TRRAP.
--- SUBCELLULAR LOCATION: Nuclear.
--- SIMILARITY: BELONGS TO THE TAF2C FAMILY.
--- SIMILARITY: Contains 1 TAFH/NHR1 domain.
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Best Local Similarity
Matches 12; Conserv
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Corticosteroid 11-beta dehydrogenase, isozyme 2 (EC 1.1.1.146) (11-DH2) (11-beta-hydroxysteroid dehydrogenase type 2) (11-beta-HSD2)
EMBL; AE016800; AA009604.1; -.

EMBL; AE016800; AA009604.1; -.

R HAMAP; MF 01808; -; 1.

InterPro; IPR00104; Phage_integrase.

R Pfam; PF02899; Phage_integrase.

R Pfam; PF02899; Phage_integrase.

R Pfam; PF02899; Phage_integrase.

W MA recombination; DNA integration; Cell division;

Chromosome partition; DNA-binding; Complete proteome.

T ACT_SITE 187 187 BY SIMILARITY.

T ACT_SITE 250 250 BY SIMILARITY.

T ACT_SITE 255 253 BY SIMILARITY.

T ACT_SITE 276 276 BY SIMILARITY.

T ACT_SITE 285 285 TRANDIENT COVALENT LINKAGE TO DNA STATESTY.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 AA; 35712 MW;
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Matches 10; Conservative
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DH12 RABIT
LD DH12 RABIT
AC P51976;
DT 01-OCT-1996
DT 01-OCT-1996
DT 10-OCT-2096
DT 10-OCT-2096
DE DH2) (11-bet.
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1 SRAHQHSMEIRTPDI------NPAWYAGRG 24 | | | : | | | : SAAHHHLAPRTPEVRAAAGALGNHVVSGSPAGAAGA 74

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316 AA

STANDARD;

RESULT 13 XERC_VIBVU ID _XERC_VIBVU

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418 AA:
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(Rel. 41, Last annotation update)
(EC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
                                                                                                                                                      STRAINS-New Zealand white; TISSUE-Kidney cortex;
STRAINS-New Zealand white; TISSUE-Kidney cortex;
MEDLINE-95269702; PubMed=7750480;
Maray-Fejes-Toth A., Fejes-Toth G.;
"Expression cloning of the aldosterone target cell-specific 11 beta-hydroxysteroid dehydrogenase from rabbit collecting duct cells.";
Endocrinology 136:579-2586(1995).
-i- FUNCTION: Catalyses the conversion of cortisol to the inactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMILERILY.
SUBCELLULAR LOCATION: Microsomal.
SUBCELLULAR LOCATION: Highly expressed in the Kidney.
SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                       Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                            metabolite cortisone. Modulates intracellular glucocorticoid
levels, thus protecting the nonselective mineralocorticoid
receptor from occupation by glucocorticoids.
CATALYTIC ACTIVITY: An 11-beta-hydroxysteroid + NAD(+) = an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 1; Length 406;
Pred. No. 23;
6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Interacts with ligand-free cytoplasmic NR3C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 BY SIMILARITY.
44181 MW; F14579663918425D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 REFLHSLRLALPDLSPVVDAITDALLAARPRPRYYPGRGL 344
NAD-dependent 11-beta-hydroxysteroid dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- WYAGRGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 AA
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STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=21092669; PubMed=11162581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, 146535; 146535.
PIR, 146535; 146535.
HSSP, 14061; 1FDU.
InterPro, 1PR002198; ADH short.
Pfam; PF00106; adh short; 1.
PROSITE; PS00061; ADH SHORT; 1.
N Oxidoreductase; NAD; Microsome.
Thub 2 11 NAD BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sialidase 3 (EC 3.2.1.18) (Membr. (N-acetyl-alpha-neuraminidase 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
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25.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            11-oxosteroid + NADH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 AA;
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Best Local Similarity
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                                                                                                                   NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity)
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28-FEB-2003
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL outstands. the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  SÜBCELLULAR LOCATION: Membrane-associated (By similarity). TISSUE SPECIFICITY: Expressed in brain, cardiac muscle and weakly
                                                         development...;
Biochem. Biophys. Res. Commun. 280:726-732(2001).
Biochem. Biophys. Res. Commun. 280:726-732(2001).

-!- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sially!

Glycoconjugates (By similarity).

-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->9)-glycosidic linkages of terminal sialic residues in cligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: Belongs to family 33 of glycosyl hydrolases.
Hasegawa T., Feijoo Carnero C., Wada T., Itoyama Y., Miyagi
"Differential expression of three sialidase genes in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 1; Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7CC46F2E5952E240 CRC64;
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By similarity.
Potential.
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Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential
Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AB026841; BAB32440.1; -. PIR, JC7588, G7588. Interpro; IPR002860; GH_BNR. Pfam; PPC2012; BNR; 3. Hydrolase; Glycosidase; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46980 MW;
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31.8%;
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Best Local Similarity 31...
7, Conservative
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us-09-700-643a/1.rag

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

sw model protein search, using OM protein August 12, 2004, 14:37:35 ; Search time 65.7849 Seconds (without alignments) 133.146 Million cell updates/sec Run on:

Title: Perfect :

US-09-700-643A-1 167 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRX 31 score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* 1: geneseqp1980s:* Database

geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

Aaw97217 Bovine pi Aaw97224 Bovine ge	2 9 0	ഥത	Aaw95184 Bovine pi Abu60829 Peptide p	۲Ü	0 bPrR	84	74 Murine	3 Murin	4 Rat 19P	3 Ra	9292 19	4 R	55	Aab90993 Prolactin
222	AAB10353 AAB10346 AAG62522	1 14 19	AAW95184 ARII60829	AAB90995	AAB73370	AAW31384	AAW95174	AAW95173	AAW87614	AAW97233	AAY49292	AAY87504	AAB10355	AAB90993
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22	2 7 7	3 7 6	18 6 18 4	35	36	37	38	ტ ტ	40	41	42	43	44	45

ALIGNMENTS

AAW31371 standard; peptide; 31 AA. AAW3137

RESULT 1

AAW31371;

(first entry) 06-APR-1998 Bovine G protein-coupled receptor ligand peptide fragment 1.

G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.

W09724436-A2 Bos taurus:

0-301-1997

96WO-JP003821. 26-DEC-1996; 95JP-00343371. 96JP-0059419. 96JP-00211805. 96JP-00246573. 28-DEC-1995; 15-MAR-1996; 12-AUG-1996; 18-SEP-1996;

(TAKE) TAKEDA CHEM IND LID.

Fukusumi Hinuma S, Habata Y, Kawamata Y, Hosoya M, Fujii R, Kitada C;

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WPI; 1997-363672/33.

N-PSDB; AAV02394.

Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland.

Claim 2; Page 160; 258pp; English.

This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 23 to 53 of the sequence in AAW31368 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a parcreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of

diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis, epplepsy and many others, also to improve postoperative nutritional status and as vasopressor. Transganic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers, to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine genome-derived ligand polypeptide fragment which is similar to the murine ligand-polypeptide

.. 0

Gaps

.. 0

Length 31; Indels

99.4%; Score 166; DB 2; I 100.0%; Pred. No. 9.2e-18; tive 0; Mismatches 0;

Best Local Similarity 100. Matches 30; Conservative

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Query Match

Sequence 31 AA;

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consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-and polyphagda, hypercholesterolaemia, hyperglyceridaemia, hyperlypidaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, rheumatoid arthritis, spinal injury, transient brain ischaemia, amylotrophic lateral sclerosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pitultary-derived ligand polypeptide; G-protein coupled orphan receptor; GRR10; UHR-1; modulator; pitultary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creuzzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                     Length 31;
                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine pituitary-derived ligand polypeptide fragment.
                                                                                                                                                                                                                                  99.4%; Score 166; DB 2; I
100.0%; Pred. No. 9.2e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                     1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                   1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                     AAW95188 standard; peptide; 31 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAR-1999 ; (first entry)
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukusumi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-009423/01
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                                                                                                                                                                                                    Sequence 31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
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This is the amino acid sequence of the bovine pituitary G protein-coupled production 1992. A method suitable for commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see AAV83792-93) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanylation followed by ammonolysis. 19P2L has prolactin secretion-stimulating and fat high doses) prolactin secretion-inhibiting properties. It can be used in the treatment and prevention of various diseases including; senile dementia, cerebrovascular dementia, and dementia associated with: Pick's disease, Huntington's disease, Parkinson's disease, Pick's disease, Parkinson's disease, Pick's disease or toxicosis (e.g. hypothyroidism, vitamin B12 deficiency, alcoholism, intoxication by
                                                                                                                                                                            19P2 ligand, G protein coupled receptor, pituitary,
prolactin releasing peptide, cattle, dementia, breast cancer, therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing a 19P2 pituitary G protein receptor ligand - by cleavage of fusion protein, useful for preventing and treating dementia, breast cancer, renal failure and autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nishimura
                                    Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanaka Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 34; 56pp; English.
                                  AAW87613 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                             97JP-00172118.
                                                                                                                                                                                                                                                                                                                                         98EP-00111725
                                                                                                                                                                                                                                                                                                                                                                                                              (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Suenaga M, Moriya T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-047884/05.
                                                                                                                                            Bovine 19P2 ligand.
                                                                                                                                                                                                                                                                                                                                         25-JUN-1998;
                                                                                                        29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                             27-JUN-1997;
                                                                                                                                                                                                                                                                                                       30-DEC-1998.
                                                                                                                                                                                                                                   Bos taurus,
                                                                                                                                                                                                                                                                   EP887417-A2
                                                                    AAW87613;
RESULT 3
                  AAW87613
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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat semile dementia; Alzheimer's, Parkinson's or Huntington's

Example 19; Page 150; 206pp; English.

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drugs, metal and organic compounds), tumourigenic diseases (e.g. brain tumour), traumatic diseases (e.g. chrcnic subarachnoidal heamcrhage, and chrebr types of dementia, depression, hyperactive child syndrome (microencephalopathy) and disturbance of consciousness. It is also useful for prevention and treatment of diseases associated with prolactin hypo pituitary adenoma, breast cancer, including; hyperprolactinaemia, pituitary adenoma, breast cancer, infertility, impotence and autoimune disease (hypersecretion disorders), and seminal vesticle hypoplasia, osteoporosis, emorpausal syndrome and renal failure (hyposecretion disorders). The 19P2 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a bovine pituitary-derived ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing hypocvarianism, genecyst cacegenesis, menopausal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine pitultary-derived ligand, modulation; prolactin secretion; G procein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Porbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abnorthal ilpidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy.
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                    99.4%; Score 166; DB 2; Length 31; 100.0%; Pred. No. 9.2e-18; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine pituitary-derived ligand polypeptide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                      1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 135; 241pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW97218 standard; peptide; 31
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                                                                                                                                                                                                                              mammalian farm animals
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                        Sequence 31 AA;
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AAW97218
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syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorrhaa, galactorrhaa, prolactinoma, infertility, impotence, amenorrhaa, galactorrhae, Forbes-Albright Syndrome, Impome, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; 19P2 ligand; diagnosis; prolactin secretion;
pituitary; regulatory mechanism; central nervous system; pancreatic.
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                                                                                                                                                                                                                                                                Length 31;
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                                                                                                                                                                                                                                                              99.4%; Score 166; DB 2; I 100.0%; Pred. No. 9.2e-18; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                           1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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Best Local Similarity 100.
Matches 30; Conservative
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                                                                                                                                                                                                                                   Sequence 31 AA;
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Sequence 31 AA;

Bovine, oxytocin secretion promoter, G protein-coupled receptor protein, treatment, disease, pain, atonic bleeding, uterine recovery failure, cow, caesarean section, artificial fertilization, galactostasis, goat, pig,

veterinary medicine; milk production

WO200038704-A1.

Bos taurus.

Bovine oxytocin secretion promoting peptide SEQ ID NO: 3.

(first entry)

24-NOV-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a monoclonal antibody which has a specific reaction with the part poptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with ahormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand
                                           Gaps
                                                                                                                                                                                                                                                                                               Monoclonal antibody, 19P2 ligand, diagnosis, prolactin secretion, pituitary; regulatory mechanism; central nervous system; pancreatic.
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              Length 31;
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                                         0; Indels
           Score 166; DB 3; I
; Pred. No. 9.2e-18;
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100.0%; Pred. No. 9.2e-18;
ive 0; Mismatches 0;
99.4%; Scc. No. ... 100.0%; Pred. No. ... 0; Mismatches
                                                                      1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
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                                                                                                                                                                            AAY49290 standard; peptide; 31 AA
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                                                                                                                                                                                                                                                                   19P2 ligand peptide fragment.
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                                           Conservative
       Query Match
Best Local Similarity
Matches 30; Conserv
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                            RESULT 6
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Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.

Claim 3; Page 50; 72pp; Japanese

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Matsumoto H, Kitada C, Hinuma

WPI; 2000-452298/39.

(TAKE) TAKEDA CHEM IND LID.

99WO-JP007199 98JP-00369585

22-DEC-1999; 25-DEC-1998;

06-JUL-2000.

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                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of frugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, therine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cow; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
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0; Indels

30; Conservative

AAB10347 standard; peptide; 31 AA

RESULT 7
AAB10347
ID AAB1
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AC AAB1

AAB10347

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Wakefulness; sleep disorder; prolactin releasing peptide receptor; PrRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea; insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure; anticonvulsant;
                                                                                                                                                                              G protein receptor ligand or peptide for controlling corticotropin
                                                                                                                                                                                                                                                    The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating disease associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoarencorticism, Addison's disease (including boredom, nauses, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening for compounds useful for promoting wakefulness or sleep, ar
for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 99.4%; Score 166; DB 4; Length 31; I Similarity 100.0%; Pred. No. 9.2e-18; 30; Conservative 0; Mismatches 0; Indels
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                                                                                                                      Hinuma S;
                                                                                                                                                                                                                               Claim 3; Page 63; 90pp; Japanese.
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             17-NOV-2000; 2000WO-JP008119.
                                         18-NOV-1999; 99JP-00327900.
26-SEP-2000; 2000JP-00297073.
                                                                                                                                                                                                releasing hormone secretion.
                                                                                       (TAKE ) TAKEDA CHEM IND LID.
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                                                                                                                      Matsumoto H,
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                                                                                                                                                   WPI; 2001-355552/37
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                        nvention
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Gaps ..

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The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PrRP) receptor (GPR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. Preceptor agonists may be used to treat common disorders which lead to sleepiness, e.g. sleep appose, narcolepsy, idiopathic hypersomnia and psychogenic hypersomnia. PrRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep disorder and psychophysiologic insomnia. The present sequence is bovine prRP-31 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide
comprises administering a prolactin releasing peptide agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
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ilarity 100.0%; Pred. No. 9.2e-18;
Conservative 0; Mismatches 0;
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                                                         24; 35pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU60825 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-2001; 2001JP-00147341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2002; 2002WO-JP004735.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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gene recombination
                                                           Disclosure; Page
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 31 AA;
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Best Local Simil
Matches 30; C
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ABU60825
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G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic;

therapeutic agent

W09724436-A2

10-JUL-1997

Bovine G protein-coupled receptor ligand peptide fragment 2.

(first entry)

06-APR-1998

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Gaps

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AAW31372 standard; peptide; 32 AA.

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The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by the gene recompination technique through tandem repeats to provide a precursor protein with specific cleavage sites, with this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
                                                                                                                                                                                                                                                                                                                                                                                                            Peptide production by gene recombination associated peptide #15
                                                                                                                                                                                                                                                                                                                                                                                                                                              production; low-molecular peptide; KiSS-1; GPR8 ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.4%; Score 166; DB 6; Length 31; 100.0%; Pred. No. 9.2e-18; ive 0; Mismatches 0; Indels
                                                                                                           Length 31;
                                                                                                       99.4%; Score 166; DB 6; Length 31 100.0%; Pred. No. 9.2e-18; ive 0; Mismatches 0; Indels
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                                                                                                                                                                             1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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                                                                                                   Query Match
Best Local Similarity 100.0
Matches 30, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene recombination
                                                                       Sequence 31 AA;
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R, Fukusumi S;

Habata Y, Kawamata Y, Hosoya M, Fujii

(TAKE) TAKEDA CHEM IND LTD.

WPI; 1997-363672/33.

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Hinuma : Kitada (

N-PSDB; AAV02395

95JP-00343371. 96JP-00059419. 96JP-00211805. 96JP-00246573.

28-DEC-1995; 15-MAR-1996; 18-SEP-1996;

.2-AUG-1996;

96WO-JP003821.

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This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 23 to 54 of the sequence in AAW13168 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper-lipidaemia, hyperrholactinaemia, diabetes, hyper-lipidaemia, hyperrholactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, cancer, pancreatitis, spinal injury, transient brain ischaemia, amylotrophic lateral scherosis, aucute myocardial infarction, spinocerbellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein
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AAW95189 standard; peptide; 32 AA.

RESULT 13 AAW95189 ID AAW95

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Gaps

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1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30

RESULT 12

30; Conservative

Local Similarity

Query Match

(first entry)

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Bovine, oxytocin secretion promoter, G protein-coupled receptor protein, treatment, disease; pain; atonic bleeding; uterine recovery failure; cow caesarean section; artificial fertilization; galactostasis; goat; pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
                                                                                                      Bovine oxytocin secretion promoting peptide SEQ ID NO:
                                                                                                                                                                                                   veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 51; 72pp; Japanese
AAB10348 standard; peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matsumoto H, Kitada C, Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-452298/39.
                                                                                                                                                                                                                                                                         WO200038704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      (TAKE ) TAKEDA
                                                                                                                                                                                                                                                                                                                                                 22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                   25-DEC-1998;
                                                                     24-NOV-2000
                                                                                                                                                                                                                                                                                                              06-JUL-2000.
                                                                                                                                                                                                                                    Bos taurus.
                                  AAB10348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated CDR10 (human) or UHR-11 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant the ligand polypeptide encoding DNA are used to produce a recombinant content of the pituitary, central nervous system, pancreas and other tissues and can be used to screen in particulary, central nervous system, pancreas and other tissues and to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's disease; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; claseases; creutzfeld-Jakob disease; poisoning by heavy metals or cancer; rheumatoid arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to carrying the ligand polypeptide encoding DNA or its mutein are used to disease, for drug screening and as source of cell lines. The ligand colypeptide source of cell lines, to identify crelated sequences; in receptor-binding assays; for production of Abb and antisera; in drug development; for gene therapy and to develop transgenic annimals. The present sequence represents a bovine genome-derived ligand colypeptide fragment which is similar to the murine ligand-polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening.
                                                                                                                        Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapputic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; davig; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
                                                                                       Bovine pituitary-derived ligand polypeptide fragment.
                                                                                                                                                                                                                                      gene therapy; transgenic animal; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 19; Page 150; 206pp; English
                                                                                                                                                                                                                                                                                                                                                                                     98WO-JP001923.
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                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hinuma S, Fukusumi S;
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                   AAW95189
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98JP-00369585. CHEM IND LTD. weak

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This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cow; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                             99.4%; Score 166, DB 3; Length 32; 100.0%; Pred. No. 9.6e-18; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine CRH releasing protein related peptide SEQ ID NO: 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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Best Local Similarity
                                                                                                                                                                                                                                                                                   Sequence 32 AA;
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                                                                                                                                                                                                                                        promoter
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Gaps . 0

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DB 2; Length 32;

99.4%; Score 166; DB 2; I 100.0%; Pred. No. 9.6e-18; 100.0%; Prec. ...

1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR

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RESULT 14 AAB10348

Conservative

Similarity

Query Match Best Local Simil Matches 30;

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Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion.
                                                                                                                                                                                                                                                                                                                                                     The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypodarenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adread gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                     Disclosure; Page 64; 90pp; Japanese.
                                                                                                                                                                                               Kitada C, Matsumoto H, Hinuma S;
                                                                                                      18-NOV-1999; 99JP-00327900.
26-SEP-2000; 2000JP-00297073.
                                                                    17-NOV-2000; 2000WO-JP008119.
                                                                                                                                                           (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                 WPI; 2001-355552/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32 AA;
WO200135984-A1
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Query Match
99.4%; Score 166; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.6e-18;
Matches 30; Conservative 0; Mismatches 0; Indels 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30 qq ઠે

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Gaps ;

Search completed: August 12, 2004, 14:43:53 Job time : 65.9099 secs

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RESULT 1
US-09-932-161-13
                                                                                                                                                                                                                                                August 12, 2004, 14:49:10 ; Search time 54.7907 Seconds (without alignments) 177.617 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/DCT_NEW PUB.Depp:*

2: /cgn2_6/ptodata/2/pubpaa/DCT_NEW PUB.Depp:*

3: /cgn2_6/ptodata/2/pubpaa/DCT_NEW PUB.Depp:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.Dep:*

5: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.Dep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.Dep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.Dep:*

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11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.Dep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.Dep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.Dep:*

14: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.Dep:*

15: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.Dep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.Dep:*

17: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.Dep:*

18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.Dep:*

19: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.Dep:*

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13: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.Dep:*

14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.Dep:*

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16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.Dep:*

17: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.Dep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-700-643A-1
167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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		US-09-932-161-13	US-10-044-592-	US-10-096-777-1	US-10-044-592-40	US-10-044-592-41	US-10-044-592-28	US-10-044-592-3	US-10-044-592-82	US-10-044-592-84	US-10-044-592-86	US-10-044-592-88	US-10-044-592-26	JS-09-932-161-14	US-10-044-592-	US-10-044-592-
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US-10-096-777-14	-10-044-592-	US-10-044-592-1	-10-044-592-	0-044-592-		-10-096-777-	US-10-044-592-92	-10-0	0-044-592-	-932-161-1	0-044-592-	0-096-77	-10-044-59	-10-044-5	1-1	4-592-	3-10-096-777-	9-932-161-1	10-096-777-1	92	US-09-820-155-2	-10-044-592-	1-8	-09-820-15	US-10-424-599-153474	-10-369-493-	10-424-599-	-10-108-91	US-10-424-599-268092
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16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

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Patent No. US202039333A1

Sequence 13, Application US/0993161

Sequence 13, Application US/0993161

Sequence 13, Application US/0993161

SEQUENCANT: Civelli, Olivier

APPLICANT: Civelli, Olivier

TITLE OF INVENTION: Screening and Therapeutic Methods For

TITLE OF INVENTION: Screening and Therapeutic Methods

CURRENT APPLICATION NUMBER: US/09/532,161

CURRENT APPLICATION NUMBER: US 09/560,915

PRIOR PILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 13

LENGTH: 31

TYPE: PRT

COFFANISM: Bos taurus

US-09-932-161-13

QUETY MATCH

Best Local Similarity 100.0%; Pred. NO. 8.9e-17;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps

OV

1 SRAHQHSMEIRTPDINPAWYAGRGIRPUGR 30

NUMBER OF SEQ 19

SEQUENCE 39, APPLICATION: SCROOLING SEQUENCE 18

SEGUENCE 39, APPLICATION: SCROOLING SEQUENCE 39

SEGUENCE 11 SRAHQHSMEIRTPDINPAWYAGRGIRPUGR 30

SEGUENCE 31 SEXEMALINE SECUENCE SEQUENCE 30

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SEGUENCE 31 SEXEMALION: SEQUENCE 30

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SEGUENCE 31 SEXEMALION: SEQUENCE 30

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PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 40
LENGTH: 32
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Publication No. US20020143152A1
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 30; Conservative
                                                                                                                                                                                                                                                       Best Local Similarity
Matches 30; Conserv
                                                                                                                                            TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bovine
                                                                                                                                                                                      US-10-044-592-40
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APPLICANT: Civelii, Steven
TITLE OF INVENTION: Relating To Prolactions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)
FILE REPERBNE: P. UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR PILING DATE: 2002-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 31
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; Sequence 40. US20020143152A1
; Publication No. US20020143152A1
; Pablication No. US20020143152A1
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hinuma, Shuji
; TILE OF INVENTION: Polypeptides, their Production and Use
; FILE REFERENCE: 2463102P
; CURRENT APPLICATION NUMBER: US 09/403639
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR FILING DATE: 1999-25-10
; PRIOR FILING DATE: 1998-04-27
                                                                                                                                                                                                                                                                                                                                                                                                               Length 31;
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TITLE OF INVENTION: Polypeptides, their Production and Use FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR PLING DATE: 1999-25-10
PRIOR PELICATION NUMBER: US/403639
PRIOR PELICATION NUMBER: DET/4D98/01923
PRIOR PELICATION NUMBER: PCT/4D98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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100.0%; Pred. No. 8.9e-17;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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Best Local Similarity 100
Matches 30; Conservative
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Best Local Similarity
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ORGANISM: Bos taurus
US-10-096-777-13
                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-39
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US-10-044-592-40
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US-10-096-777-13
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SEQ ID NO 39
LENGTH: 31
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APPLICANT: FRUGUMI, Shuji
APPLICANT: FRUGUMI, Shoji
TITLE OF INVENTION: POlypeptides, their Production and Use;
FILE REPRENCE 2453US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT PILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR APPLICATION NUMBER: UP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 28
99.4%; Score 166; DB 13; Length 32;
llarity 100.0%; Pred. No. 9.2e-17;
Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 9.5e-17;
iive 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-86
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; ORGANISM: Bovine
US-10-044-592-84
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US-10-044-592-86
Query Match
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US-10-044-592-82

Sequence 82, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Himma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use

TITLE OF INVENTION: Polypeptides, their Production and Use

TITLE OF INVENTION: 2463USD

CURRENT FILING DATE: 2653USD

CURRENT FILING DATE: 2002-01-10

PRIOR FILING DATE: 1999-25-10

PRIOR PELING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: PCT/UP98/01923

PRIOR PELING DATE: 1997-04-28

NUMBER OF SEQ ID NOS: 96

LENGHARE:

SEQ ID NO 82

LENGHH: 98

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US-10-044-592-38

Publication No. US20020143152A1

Publication No. US20020143152A1

APPLICANT: Hinuma, Shuji

APPLICANT: Hinuma, Shuji

APPLICANT: Hinuma, Shuji

ITILE OF INVENTION: Polypeptides, their Production and Use

FILE REFERENCE: 2463US2P

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 2002-01-10

PRIOR APPLICATION NUMBER: US 09/403639

PRIOR APPLICATION NUMBER: US 09/403639

PRIOR APPLICATION NUMBER: US 09/403639

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR PILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-27

NUMBER OF SEQ ID NOS: 96
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                                                                                                  Query Match 99.4%; Score 166; DB 13; Length 98; Best Local Similarity 100.0%; Pred. No. 3e-16; Matches 30; Conservative 0; Mismatches 0; Indels
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Matches 30; Conservative
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Murine
US-10-044-592-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
// ORGANISM: Bovine
US-10-044-592-82
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ORGANISM: Bovine
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SOFTWARE:
SEQ ID NO 38
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Sequence 84, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Eukusumi, Shoji
ITILE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION WUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: PCT/UP98/01923
PRIOR APPLICATION NUMBER: PCT/UP98/01923
PRIOR APPLICATION NUMBER: PCT/UP98/01923
PRIOR APPLICATION NUMBER: US/25-10
PRIOR APPLICATION NUMBER: US/25-10
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-28

SOFTWARE:
SEQ ID NOS: 96

SOFTWARE:
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SCHELL INFORMATIONS:
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
ITILE OF INVENTION: Polypeptides, their Production and Use
FILE REPERENCE: 2453452
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1099-25-10
PRIOR APPLICATION NUMBER: DCJ/JP98/01923
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-45-7
PRIOR FILING DATE: 1999-6-4-7
PRIOR FILING DATE: 1999-6-6-5
SEQ ID NOS: 96
LENGTH: 98
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Pred. No. 3e-16,
0, Mismatches 0, Indels
99.4%; Score 166; DB 13; Length 98; 100.0%; Pred. No. 3e-16; o; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
99.4%; Score 166; DB 13;
Best Local Similarity 100.0%; Pred. No. 3e-16;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                30
                                                                                                                                                           23 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.4%; Sc
Best Local Similarity 100.0%; P
Matches 30; Conservative 0;
                         Best Local Similarity 100.0
Matches 30, Conservative
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Sequence 4, Application US/10044592

Sequence 4, Application US/10044592

Publication No. US20020141152A1

GENERAL INPORMATION:

APPLICANT: Hinna, Shuji

APPLICANT: Hinna, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2454052P

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 1999-25-10

PRIOR FILING DATE: 1999-25-10

PRIOR FILING DATE: 1998-04-10

SEQ ID NOS: 96

SOFTWARE:

SEQ ID NOS: 96

SEQ ID NOS: 96
                  Sequence 14, Application US/09932161
Patent No. US20020037533A1
GENERAL INFORMATION:
APPLICANT: Civeli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: PCC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR PELICATION NUMBER: US 09/560,915
PRIOR APPLICATION NUMBER: US 09/560,915
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 31;
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Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinner, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 157; DB 13;
Pred. No. 1.8e-15;
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94.0%; Score 157; DE
Best Local Similarity 93.3%; Pred. No. 1.8e
Matches 28; Conservative 0; Mismatches
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Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Rattus
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                                                                                                                APPLICANT: HORMATION:
Sequence 89, Application US/10044592
Sequence 89, Application US/10044592
Sequence 80, Development of the publication of USC020143152A1
GENERAL INFORMATION:
APPLICANT: FUREUMI, Shuji
APPLICANT: FUREUMI, Shoji
ITILE OF INVENTION: Polypeptides, their Production and Use FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 88
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:
APPLICANT: Hinuma. Shuji
APPLICANT: Hinuma. Shuji
APPLICANT: Fukusumi, Shoji
ITIE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2563UG2P
CURRENT FILING DATE: 2999-25-10
PRIOR APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-04-27
PRIOR PLING DATE: 1999-04-27
PRIOR PLING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
SOFTWARE:
SOFTWARE:
SOFTWARE:
SOFTWARE:
SEQ ID NOS: 96
LENGTH: 29
TYPE: PRI
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96.4%; Score 161; DB 13;
Best Local Similarity 100.0%; Pred. No. 4.4e-16;
Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
99.4%; Score 166; DB
Best Local Similarity 100.0%; Pred. No. 3e-
Matches 30; Conservative 0; Mismatches
23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Bovine
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US-10-044-592-26
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US-10-044-592-26
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RESULT 13

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CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 2002-01-10

PRIOR FILING DATE: 1999-25-10

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1997-04-28

CONTAMRED OF SEQ ID NOS: 96

CONTAMRED OF SEQ ID NOS: 96

CONGANISM: Artificial Sequence

FEATURE: PETTURE

CORGANISM: Artificial Sequence

PRIOR FILING

CONGANISM: Artificial Sequence

CONGANISM: Artificial Sequence

CONGANISM: Artificial Sequence

PRIOR FILING

CONGANISM: Artificial Sequence

CONGANISM: Artif
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Search completed: August 12, 2004, 15:22:49 Job time : 54.7907 secs

Sequence Seq

Sequence Sequence Sequence 137

Sequence Sequence Sequence Sequence Sequence

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Sequence 7, Application US/09105678A

Sequence 7, Application US/09105678A

Patent No. 610382

GENERAL INFORMATION:
APPLICANT: Suchaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.4%; Score 166; DB 3; Length 31; 100.0%; Pred. No. 9.5e-19; ive 0; Mismatches 0; Indels
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US-09-421-208-37
US-09-560-11-14
US-09-799-955-4
US-09-105-678A-38
US-08-77-208-39
US-09-105-678A-39
US-09-105-678A-39
US-09-105-678A-39
US-08-776-971-49
US-08-776-971-124
US-08-776-971-124
US-08-776-971-137
US-08-776-971-137
US-08-776-971-137
US-08-776-971-137
US-08-105-678A-9
US-09-105-678A-9
US-09-105-678A-9
US-09-105-678A-9
US-09-105-678A-9
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Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
      TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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STATE: MA
COUNTRY: USA
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US-09-105-678A-7
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Sequence 31, App
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                                                                                        August 12, 2004, 14:37:36; Search time 17.6628 Seconds (without alignments) 90.609 Million cell updates/sec
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1. /GghZ = 6/ptodata/2/iaa/5A_COMB.pep:*

2. /GgnZ = 6/ptodata/2/iaa/6B_COMB.pep:*

3. /GgnZ = 6/ptodata/2/iaa/6A_COMB.pep:*

3. /GgnZ = 6/ptodata/2/iaa/6B_COMB.pep:*

5. /GgnZ = 6/ptodata/2/iaa/PGTUS_COMB.pep:*

5. /GgnZ = 6/ptodata/2/iaa/PGTUS_COMB.pep:*

5. /GgnZ = 6/ptodata/2/iaa/PGTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGRX 31
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US-08-776-971-5
US-09-421-208-7
US-09-421-208-7
US-09-56-915-13
US-09-105-678A-32
US-09-105-678A-32
US-09-105-678A-32
US-09-105-678A-32
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                          Perfect score:
                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                   Searched:
                                                                                           Run on:
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No.
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Gaps

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Kiteda, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
STREET: 130 Water Street
STREET: 130 Water Street
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 31;
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                                                                                                                                COMPUTEY: USA

COMPUTER RADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <u >Unknown><u >Unknown><u >Usasien</u>
CLASSIFICATION: <u >Unknown><u >Usasien</u>
CLASSIFICATION: <u >Unknown><u >Usasien</u>
CLASSIFICATION: <u >Unknown><u >Unknown><u >Usasien</u>
CLASSIFICATION: <u >Unknown><u >Unknown><u >Usasien</u>
CLASSIFICATION: <u >Unknown><u >Usasien</u>
CLASSIFICATION: <u >Unknown><u >Unknown><u >Unknown><u >Usasien</u>
CLASSIFICATION: <u >Unknown><u >Usasien</u>
CLASSIENCATION: <u >Unknown><u >Usasien</u>
CLASSIENCATION: <u >Usasien</u>
CLASSIENCATION: <u >Unknown><u >Usasien</u>
CLASSIENCATION: <u >Usasien</u>
CLASSIENCA
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Best Local Similarity 100.0%; Pred. No. 9.5e-19;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION: CURACIONARY

APPLICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 7/343371

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: JP 8/59419

FILING DATE: 18-DEC-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 12-AUG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-DEP-1996

ATTORNY/AGENT INFORMATION:

NAME: COALIN, DAVIG G.

REGISTRATION NUMBER: 27,026

REGISTRATION INFORMATION:

TELEBCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
PRAGMUT TYPE: internal
SEQUENCE DESCRIPTION: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 97, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                        STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukusumi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-776-971-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-776-971-5
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Kiteda, Chieko
INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
F SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 31;
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Masato
APPLICANT: Moziya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE: 54
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.4%; Score 166; DB 3; I Best Local Similarity 100.0%; Pred. No. 9.5e-19; Matches 30; Conservative 0; Mismatches 0;
1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-UN11998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                        Sequence 31, Application US/09105678A Patent No. 6103882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
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Fujii, Ryoʻ
----i. Shoji
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Kawamata, Yuji
Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
COUNTRY: USI
ZIP: 02109
                                                                                                                                                                                    -09-105-678A-31
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US-08-776-971-5
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Sequence 31, Application US/09421208

Sequence 31, Application US/09421208

Patent No. 625851

GENERAL INFORMATION:
APPLICANT: Stenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
APPLICANT: Mishimura, Osamu
APPLICANT: Mishimura, Osamu
ATTLE OF INVENTION: Mishimura, Osamu
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Loston
COTY: Loston
COTY: Loston
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE: Co-UN-1998
APPLICATION NUMBER: US 09/105,678
FILING DATE: 20-UN-1998
APPLICATION NUMBER: US 09/105,678
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 23,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.4%; Score 166; DB 3; I
Best Local Similarity 100.0%; Pred. No. 9.5e-19;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                FILING DATE: 26-UN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-340
TELEPHONE: 617-523-340
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
US 09/105,678
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                   LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-7
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-421-208-31
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| Sequence 7, Application US/09421208
| Patent No. 625851
| GENERAL INFORMATION:
| APPLICANT: Suemaga, Masato
| APPLICANT: Tanaka, Yoko
| APPLICANT: Thishimura, Osamu
| TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
| NUMBER OF SEQUENCES: 52
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: 130 Water Street
| CITY: Boston
| STREET: MA
| COUNTY: WA
| COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                   COMPUTER NEADMENDE NORM:
COMPUTER: IBM compatible
OOPENATING SYSTEM: DOS
SOFTWARE: FasteSQ for Windows Version 2.0
SOFTWARE: FasteSQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILLING DATE: 06-Feb-1997
CLASSIFICATION ADATA:
APPLICATION NUMBER: PCT/UP96/03821
FILLING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/34371
FILLING DATE: 13-MAR-196
APPLICATION NUMBER: JP 8/59419
FILLING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/59419
FILLING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILLING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
APPLICATION NUMBER: JP 8/211805
APPLICATION NUMBER: JP 8/246573
ATTORNEY/AGENT INFERMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

99.4%; Score 166; DB 3; I
Best Local Similarity 100.0%; Pred. No. 9.5e-19;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CONLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 97. US-08-776-971-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
                     COMPUTER READABLE FORM
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SEQUENCE CHARACTERISTICS
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-32
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ZIP: 02109
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US-08-776-971-6
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                                                                                                                                                                                                                                                                              Sequence 13, Application US/09560915

Patent No. 6383764

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

APPLICANT: Lin, Steven

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)

FILE REPRENCE: P-UC 3534

CURRENT APPLICATION NUMBER: US/09/560,915

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Mindows Version 4.0

SEQ ID NO 13

LENGTH: 31
                                                                                                             Gaps
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                                                              Query Match

99.4%; Score 166; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.5e-19;
Matches 30; Conservative 0; Mismatches 0; Indels
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Patent No. 610382
GENERAL INFORMATION:
APPLICANT: Stenaga, Masato
APPLICANT: Tanaka, Yoko
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 166; DB 4; ]; Pred. No. 9.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.4%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                              SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 100.7
Matches 30, Conservative
  peptide
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Bos taurus
US-09-560-915-13
; MOLECULE TYPE:
US-09-421-208-31
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COUNTRY: US/
ZIP: 02109
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US-09-105-678A-32
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DIKE, BRONSTEIN, ROBERIS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                Length 32;
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MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
COMPUTER: IBM compatible
SOFTWARE: FastSEO for Windows Version 2.0
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
ATTORNEY/AGENT INFORMATION:
NAME: COALIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                Query Match
99.4%; Score 166; DB 3; I
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 130 Water Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
REPERENCE/DOCKET NUMBER: 484.
TELECOMMUNICATION INFORMATION:
TELEPROME: 617-523-3400
TELEPRAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hosoya,
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 6:
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Hosoya, Masaki
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Habata, Yugo
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99.4%; Score 166; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                    Length 32;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Nanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                Query Match 99.4%; Score 166; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 9.9e-19;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                        1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                   1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECHONGUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 32 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 130 We
CITY: Boston
STATE: MA
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SRAHQHSMEIRTPDINPAWYAGRGIRPVGR

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Gaps
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSES: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
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Sequence 33. Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: ADDRESSE:
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.4%; Score 166; DB 3; Length 33; 100.0%; Pred. No. 1e-18;
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGBNT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
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Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                          CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                          COUNTRY:
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US-08-776-971-7
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Gaps
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APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Nasaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
UNUMBER OF SEQUENCES: 140
CORRESPONDENCES. 140
CORRESPONDENCES. 180
ADDRESSE: DIXE, BRONSTEIN, ROBERTS & CUSHWAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.4%; Score 166; DB 3; Length 33; 100.0%; Pred. No. 1e-18; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-MAR-1996
APPLICATION VUMBER: 3P 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                      APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/POCKET NUMBER: 48466-342
TELEPHONE: 617-523-5400
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                   FILING DATE:
REIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN 1998
APPLICATION NUMBER: UP 172118/1997
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08776971B Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
These 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-421-208-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-776-971-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                         OPERATING SYSTEM: DOS
CURRENT APPLICATION UNMBER: US/08/776,971B
APPLICATION UNMBER: US/08/776,971B
FILING DATE: O6-Feb-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
APPLICATION NUMBER: JP 8/211805
APPLICATION NUMBER: JP 8/216573
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CONLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 107-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-776-971-7
                                                                                      COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/09421208
Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 33 amino acids TYPE: amino acid
                   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UR
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US-09-421-208-33
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| Sequence 44, Application US/08776971B |
| Patent No. 6228984 |
| Patent No. 6228984 |
| APPLICANT: Hinuma, Shuji |
| Habata, Yuji |
| Hosoya, Masaki |
| Kitada, Chieko |
| Fujii, Ryo |
| Fujii, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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99.4%; Score 166; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-18;
Matches 30; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: IBM compatible
CONFUMARE: Fast SEG for Windows Version 2.0
SOFTWARE: Fast SEG if Windows Version 2.0
SOFTWARE: (96-Feb-1997
CLASSIFICATION NUMBER: (97/495/03821
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: (97/443371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 18-D86
APPLICATION NUMBER: JP 8/246573
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APTORNEY/AGENT: INFORMATION:
NAMM: COALIN: DAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 52
                                     NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: procein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-776-971-1
                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 98 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
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August 12, 2004, 14:37:36 ; Search time 13.6977 Seconds (without alignments) 217.697 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                            ints satisfying chosen parameters:
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1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRX
                                                                                                                                                                                                                                                                                                               283366 segs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 200000000
                                                                                                                                                                                  US-09-700-643A-2
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                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB
Maximum DB
                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote hypothetical prote probable regulator hypothetical prote hypothetical prote hypothetical prote hypothetical prote dynein beta heavy hypothetical prote hypothetical prote hypothetical prote lipopolysaccharide hypothetical prote probable aldC prot hypothetical prote N-acetylglutamate hypothetical prote Sun/nucleolar prot segmentation prote ubiquinone biosynt hypothetical prote sensory box histid probable glutathio hypothetical prote hydroxybenzoate oc prolactin-releasin hypothetical prote conserved hypothet glutathione S-tran sensory transducti Description JC7607 F83376 B9376 D87559 D87559 T47959 F69099 S67150 S76955 S67150 C83292 C83292 C83292 C83392 T3759 D70885 A97446 A82193 A33111 G82669 B87577 F71015 H82852 T48336 C84480 T14914 AB2664 303 118 220 335 348 455 Length 345 393 401 Query ии 4 4 и 6 2 4 · · иииии 4 4 4 4 4 4 4 4 8 иии 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 2.7.4 47.5 47.5 47.5 47.5 Score Result No.

probable 1-acylgly	related to BCS1 pr	hypothetical prote	densin-180 - rat	hypothetical prote	genome polyprotein	ALR protein - huma	ALR protein - huma	probable lpgR prot	malic acid transpo	malic acid transpo	hypothetical prote	hypothetical prote	hypothetical prote	glutamate-ammonia-	Mg protoporphyrin
D64688	T49717	A84089	T31434	T13250	MINIWINE	T03455	T03454	F70812	B64395	H64371	AH3166	A12516	T39050	H87112	T50904
0	7	7	~	~	H	7	7	0	7	7	7	N	~	~	0
240	779	957	1495	1607	1693	4957	5262	256	342	347	419	689	698	1004	1236
28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	27.7	27.7	27.7	27.7	27.7	27.7	27.7	27.7
'n	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46	46	46	46	46	46	46	46
46															

ALIGNMENTS

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projection-releasing peptide - rat

C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: JC7607
R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T.
Bjochem. Biophys. Res. Commun. 281, 53-56, 2001
A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: Mul
A;Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen
A;Accession: JC7607
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83376
C;Accession: F83376
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Badman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jory, S.; Olson, M.V.
Nature 406, 959-954, 2000
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-664 <STO>
A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 25; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 33/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Genetics:
A;Gene: PA2151
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A,Gene: PrRP
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DB 2; Length 664;

34.0%; Score 56.5;

N

Indels

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4; Mismatches

Similarity 45.8%; 11; Conservative

Best Local Matches 1

470 YRPNFFVNTPDINP-WFLQRSGRP 492

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HRHSMEIRTPDINPAWYASRGIRP 27

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47959
R;De Haan, Marse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet: submitted to the Protein Sequence Database, January 2000
A;Reference number: Z24480
A;Accession: T47959
A;Accession: T47959
A;Accession: T47959
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: Logo, cDEH>
A;Residues: 1-790, cDEH>
A;Experimental source: cultivar Columbia; BAC clone F15G16
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Eur. J. Biochem. 221, 101-109, 1994

Eur. J. Biochem. 221, 101-109, 1994

A;Title: Cloning, sequencing and expression of the gene encoding the coenzyme B(12)-deper A;Reference number: 543237; MUID:94222050; PMID:8168499

A;Accession: S77900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Methanobacterium thermoautotrophicum circles. Methanobacterium thermoautotrophicum c;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C;Accession: F69099 #sequence of Methanobacterium thermoautotrophicum Delta H: funct: A;Accession: F69099 #MID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: GB:AE000805, GB:AE000666, NID:g2621213, PIDN:AAB84680.1, PID:g262121
A,Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain Del
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 1 - Clostridium barkeri (fragment)
C;Species: Clostridium barkeri
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 05-Nov-1999
C;Accession: S77900; S43551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X77484; NID: 9472895; PIDN: CAA54624.1; PID: 9472896
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Pred. No. 12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52;
Pred. No. 1
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A;Introns: 39/1; 678/2; 698/3; 773/2
A;Note: F15G16.60
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Best Local Similarity 55.6%;
Matches 10; Conservative
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ilarity 46.4%;
Conservative
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Best Local Similarity
Matches 13; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
A; Molecule type: DNA
> Peridues: 1-123 <BEA>
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A,Gene: MTH174
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: D87559
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolato, M.T.; Databerg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Reference number: A87249; MUD:21173698; PMID:11259647
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                       hypothetical protein Rv3485c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Natures 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atlie: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: B70569
A;Accession: B70569
A;Accession: B70569
A;Residues: 1-314 <COL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:Z95390; GB:AL123456; NID:g3261766; PIDN:CAB08708.1; PID:g2104408
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: Rv3485c
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;46-227/Domain: short-chain alcohol dehydrogenase homology <8ADH>
                                                      ä
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A,Residues: 1-637 <STO>
A,Cross-references: GB:AE005673; NID:g13424056; PIDN:AAK24472.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC2501
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48.0%; Pred. No. 9.7;
iive 4; Mismatches 9; Indels
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11; Indels

5, Mismatches Score 53.5; Pred. No. 3.

ch 32.2%; l Similarity 27.5%; ll; Conservative

Best Local Similarity

Matches

5; DB 2; 3.8;

1 SRTHR-------HSMEIRTPDINPAWYASRGIRP 27

g

8

D87559

hypothetical protein F15G16.60 - Arabidopsis thaliana

RESULT 5 T47959

4 HRHSMEIRTPDINPAWYASRGIRPV 28

Local Similarity 48.0 es 12; Conservative

Query Match

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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno A;Accession: E91002
A;Reference number: A99629; NUID:21156231; PMID:11258796
A;Reference number: A99629; NUID:21156231; PMID:11258796
A;Residue: preliminary
A;Residues: 1-72 cHAY>
A;Reperences: GB:BA000007; PIDN:BAB36412.1; PID:gl3362458; GSPDB:GN00154
A;Reperences: GE:BA000007; PIDN:BAB36412.1; PID:gl3362458; GSPDB:GN00154
A;Gene: EC52989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apporbetical protein all1686 [imported] - Nostoc sp. (strain PCC 7120)
hypothetical protein all1686 [imported] - Nostoc sp. (strain PCC 7120)

6;Species Nostoc sp. PCC 7120

6;Species Nostoc sp. strain PCC 7120

6;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 24-Nov-2003

6;Accession: AH2016

8;Kaneko, T.; Nakamira, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Accession: AH2016

A;Accession: AH2016
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AG3169
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
Frapp, Pr.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2277; MUID:21608550; PMID:11743193
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A;Cross-references: GB:BA000019; PIDN:BAB78052.1; PID:g17135506; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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A;Cross-references: GB:AE008687; PIDN:AAL45769.1; PID:g17743503; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
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C;Superfamily: tartrate-resistant acid phosphatase
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Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 HRHSMEIRTPDINPAWY----ASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB
Pred. No. 3.5;
5; Mismatches
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34.5%;
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Best Local Similarity 34.54
Matches 10, Conservative
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Best Local Similarity 48.49
Matches 15, Conservative
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A;Molecule type: DNA
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A, Molecule type: DNA
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NyAlternate names: hypothetical protein 05315
C\Specias: Saccharomyces cerevisiae
C\Specias: Saccharomyces cerevisiae
C\Specias: Saccharomyces cerevisiae
C\Spacession: S67150
R\Jauniaux, Jr.C.; Pointey, R.
Submitted to the Protein Sequence Database, July 1996
A\Reference number: S67143
A\Rolecule type: DNA
A\References: EMBL: Z75161; NID:g1420572; PID:e252411; PID:g1420573; GSPDB:GN00015;
A\Rolecule type: DNA
A\Respectmental source: strain S288C
C\Genetics:
A\Genetics:
A\Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                CiSpecies: Synechocystis sp.
A; Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: 876555
R;Raneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; R,; Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA, Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIN
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                                                           1;
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                                                       Indels
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                                                           12;
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Pred. No. 7.8;
7; Mismatches 13;
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                                                                                                                          ---INPAWYASRGIRPVGR
                                                                                                                                                                                         73 RTHYGAMEVRIPDAPKCNEÍVVÁLVFSNGGRPHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
30.1%; Score 50; DB 2
Best Local Similarity 33.3%; Pred. No. 4.6;
Matches 11; Conservative 6; Mismatches
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                      Pred. No. 4.4;
2; Mismatches
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Best Local Similarity 28.1%;
Matches 9; Conservative
                  42.9%;
                                                       Conservative
                                                                                                                          2 RTHRHSMEIRTPD---
                  Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein -
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A;Cross_references: EMBJ:Z81074; PIDN:CAB03039.1; GSPDB:GN00022; CESP:F32B6.3
A;Experimental source: clone F32B6
C;Genetics:
                                                                                                                                                     C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T21648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: 4
A,Introns: 56/3; 105/1; 146/3; 185/1; 223/1; 258/2; 320/3
                                                                                                          hypothetical protein F32B6.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                    R)Basham, V. submitted to the EMBL Data Library, October 1996 A)Reference number: 219453 A)Rocesion: T21648 A)Accession: T21648 A)Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: August 12, 2004, 14:50:26 Job time : 14.6977 secs
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112 RKRLHQLELAQPDLNEGW 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.9%;
Best Local Similarity 38.9%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable glutathione S-transferase PA2821 [imported] - Pseudomonas aeruginosa (strain PA Cispecies: Pseudomonas aeruginosa (cispecies: Pseudomonas aeruginosa (cispecies: Pseudomonas aeruginosa (cispecies: Psep-2000 #sequence_revision 15-Sep-2000 #text_change 23-Mar-2001 Cispecies: O.83292 Msequence_revision 15-Sep-2000 #text_change 23-Mar-2001 Cispecies: C.8.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brandan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V. Alture 406, 959-964, 2000 Alture 406, 959-964, 2000 Alture 406, 959-964, 2000 Alture 408. Alture 406, 959-964, 2000 Alture 408. Presidence of Pseudomonas aeruginosa PA01, an opportunistic patholy. Alterence number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-220 <STO>
A;Residues: 1-220 <STO>
A;Cross-references: GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAGG6209.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2821
C;Superfamily: plaice glutathione transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipopolysaccharide heptosyltransferase (EC 2.4.99.-) I rfaC (similarity) - Bordetella pe
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                                                                                                                                                     Score 48; DB 2; Length 118;
Pred. No. 8.4;
5; Mismatches 12; Indels
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Pred. No. 17;
3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 2; Length 335; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
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C;Superfamily: heptosyltransferase I
C;Keywords: glycosyltransferase
                                                                                                                                                     Query Match 28.9%;
Best Local Similarity 34.4%;
Matches 11; Conservative
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1 Similarity 44.0%;
11; Conservative
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nilarity 43.5%;
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Best Local Similarity
Matches 10, Conserv
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                                  A;Gene: Atu5077
A;Genome: plasmid
C; Genetics:
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Length 348; 8; Indels

Score 48; DB 2; Pred. No. 27; 3; Mismatches

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRX 31
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Y587_PASMU.
NER3_BOVIN
ARGC_BACHD
CNC_DROME
EX71_STRCO
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                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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P18897 rattus norv	P77562 escherichia	P54974 agrobacteri	P30143 escherichia	P31795 radiation m	P17812 homo sapien	P32770 saccharomyc	P03357 akr murine	Q9uia9 homo sapien	Q9epk7 mus musculu	P03356 akv murine	P11227 radiation m
SMR2_RAT	YAIW_ECOLI	CRTY_AGRAU	YAAJ_ECOLI	POL MLVRK	PYRG HUMAN	NRP1 YEAST	POL MLVAK	XPO7 HUMAN	XPO7 MOUSE	POL MLVAV	POL_MLVRD
7 1	4	9	1 9	1 1	1	1	3 1	7 1	7 1	1 9	9
137	36	38	47	58	59	71	84	108	108	119	119
26.5	26.5	26.5	26.5	26.5	26.5	26.5	26.5	26.5	26.5	26.5	26.5
44	44	44	44	44	44	44	44	44	44	44	44
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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PRESULT I
PRESULT I
PREPRINTAN
PROJECTION (Rel. 39, Created)

DE 30-MAY-2000 (Rel. 39, Created)
DE 70-MAY-2000 (Rel. 41, Jack monctation update)
DE 70-MAY-2010 (May 10, May 10,
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Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP20].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83:1-10(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative splicing.
$10ML 1 21
PEPTIDE 22 52
PEPTIDE 33 52
PROPEP 57 83
MOD RES 52
VARŠPLIC 33 83
                                                                                                                                                                                                                                        Nature 393:272-276(1998)
                                                                Rattus norvegicus
                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pept.
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-!- TISSUB SPECIFICITY: Medulla oblongata and hypothalamus.
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                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-RAY-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                          Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION (G-54 PROVIDE AMIDE GROUP). 08AC35A13B0FA908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fukusumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
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Hormone; Amidation; Signal; Cleavage on pair of basic residues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fuk
Kitdda C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-relaesing peptide in the brain.";
Nature 393:272-276(1998).
                 Score 165; DB 1; Length 87;
Pred. No. 5.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 152; DB 1; Length 98;
Pred. No. 5.7e-16;
1; Mismatches 2; Indels
                                              0; Indels
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PRRP RAT
AC P81278; Q8K3Y0;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
       99.4%; Scor.
100.0%; Pred. No. 5.-
                                                                                                                                                                               98 AA.
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1; Mismatches
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                                                                                            SRTHRHSMEIRTPDINPAWYASRGIRPVGR
                                                                              SRIHRHSMEIRTPDINPAWYASRGIRPVGR
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MEDLINE=98268781; PubMed=9607765;
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10544 MW;
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Local Similarity 90.0%;
les 27; Conservative
Query Match
Best Local Similarity 100...
"hes 30; Conservative
                                                                                                                                                                                                                                                                                    releasing peptide PrRP20]
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Matches
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DATE THE STANDARD COURT OF THE STANDARD COUR

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION (G-53 PROVIDE AMIDE GROUP).
TPDINPAWYTGRGIRPVGRPGRRRATPRDVTGLGQLSCLPL
DGRTKFSQRG -> SECLTYGRQPLISFHPFTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lattetrophs directly to secrete PRL.

ALTERNATIVE PRODUCTS:
Rattus Muregitus (rat).
Ekkaryota, Meteria, Chodata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=99426652; PubMed=10498338;
Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sumino Y., Fujino M.; "Tissue distribution of prolactin-releasing peptide (PrRP) and its
                                                                                                                                                                                TISSUE=Brain;
MEDLINE=98269'81; PubMed=9607765;
Hinuma S., Habara Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=P81278-2; Sequence=VSP_004370;
TISSUE SPECIFICITY: Widely expressed, with highest levels in
medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JC7607; JC7607.
Hormone; Amidation; Signal; Cleavage on pair of basic residues;
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Pred. No. 1.1e-14;
1; Mismatches 4; Indels
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PROLACTIN-RELEASING PEPTIDE
PROLACTIN-RELEASING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP 004370.
D0C75A264EEE4F29 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P81278-1; Sequence=Displayed;
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                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2).
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EMBL; AF521930; AAM82154.1; -.
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Best Local Similarity 83.3%;
Matches 25; Conservative
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                                                                                                                                                                                   (Ganglioside sialidase)
                                                                                                                                                                                                                                                                                                                                         Wada T., Yoshikawa Y., Tokuyama S., Kuwabara M., Akita H., Miyagi T., "Cloning, expression, and chromosomal mapping of a human ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monti E., Bassi M.T., Papini N., Riboni M., Manzoni M., Venerando B., Croci G., Preti A., Ballabio A., Tettamanti G., Borsani G.; "Identification and expression of NEU3, a novel human sialidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoconjugates.
--- CATALNITC ACTIVITY: Hydrolysis of alpha-(2--3)-, alpha-(2--6)-, alpha-(2--8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
--- SUBCELLULAR LOCATION: Membrane-associated.
--- TISSUE SPECIFICITY: Highly expressed in skeletal muscle, testis, adrenal gland and thymus, followed by pancreas, liver, heart and thymus. Weakly expressed in kidney, placenta, brain and lung.
--- MISCELLANEOUS: Optimum ph is 3.8
--- SIMILARITY: Contains 3 BNR repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated to the plasma membrane.";
Biochem. 0. 349:343-351(2000).
-!- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 604617; -. Gintegral to plasma membrane; TAS. GO; GO:0003887; C:integral to plasma membrane; TAS. GO; GO:0003824; F:catalytic activity; TAS. GO; GO:0006689; P:ganglioside catabolism; TAS. InterPro; IPR002866; GH BNR. Pfam; PF02012; BNR; 3. Hydrolase; Glycosidase; Membrane; Repeat.
                                                                                                                        CBOG 100469; CONCEI, 20 AND CONCEI, 20 AND CBOG 200469; CONCEI, 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-BEJ 2003 (Rel. 41, Last annotation update)
(N-acetyl-alpha-neuraminidase 3)
                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 261:21-27(1999).
                                                                                                                428 AA
                30
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                                       SRAHQHSMETRTPDINPAWYTGRGIRPVGR
                SRIHRHSMEIRIPDINPAWYASRGIRPVGR
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BNR 2.
BNR 3.
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Genew; HGNC:7760; NEU3.
MIM; 604617; -.
                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
MEDLINE=99335353; PubMed=10405317;
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                                                                                                                STANDARD;
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TISSUE=Skeletal muscle;
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HUMAN
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- SIMILARITY: Belongs to the fructosamine kinase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro, IPR005581; Fructosamin kin.
Pfam, PF03881; Fructosamin kin; 1.
Hypothetical protein; Transfess, Kinase; Complete proteome.
SEQUENCE 288 AA; 33778 WW, F4D2F6C26014D940 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 288;
                                                                                                                                                                                                 Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                    35D1DD9359A78C98 CRC64;
                                                                                                                                                                                                 Score 54; DB 1;
Pred. No. 1.7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52; DB 1;
Pred. No. 2.2;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein PM0587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
              By similarity.
Potential.
Potential.
Potential.
Potential.
Potential.
By similarity.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                           288 AA.
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                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                       195 KTRPHSLMIYSDDLGVTWHHGRLIRPM 221
                                                                                                                                                                                                                                                                     2 RIHRHSMEIRTPDINPAWYASRGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHECKIHTGEMHEAWIIDDGIQPV 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 RHSMEIRTPDINPAWYASRGIRPV 28
                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE006094; AAK02671.1; -.
                                                                                                                                                                      48252 MW;
                                                                                                                                                                                                     32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.3%;
Similarity 37.5%;
9; Conservative 6
                                                                                                                                                                                                                                       Conservative
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(Rel. 41, (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                      A
B
                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
24
25
25
20
225
245
                                                                                                                                                                   428
                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 10;
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                           Y587 PASMU
Q9CN56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                ACT SITE
SEQUENCE
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NER3 BOVIN
ID NER3 BO
AC 097859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PM0587
                                                                                                                                                                                                                                                                                                                                                         RESULT 5
Y587_PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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MEDLINE-92001535; PubMed=1911393;
Mohler J., Vani K., Leung S., Epstein A.;
"Segmentally restricted, cephalic expression of a leucine zipper gene during Drosophila embryogenesis.";
Mech. Dev. 34:3-9(1991).
                                                                                                                                                                                                                                                                                                                          acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase)
ARGC OR BH1900.
                                                                                                                                                                                                                                               Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP, MF 00150; -; 1.
InterPro; IPR000706; AGPR act site.
InterPro; IPR000534; Semialdhdh.
Pfam; PF01118; Semialdhyde dh; 1.
Pfam; PF01118; Semialdhyde dh; 1.
ProDom; PD003765; AGPR act site; 1.
PROSITE; PS01224; ARGC; 1.
Arginine biosynthesis, Oxidoreductase; NADP; Complete proteome. ACT SITE 149 149 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endotterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                         ARGC OR BH2900.
Bacillus halodurans.
Bacreria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3E9F45DD09FC68EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.6%; Score 47.5; D
45.5%; Pred. No. 13;
iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         533
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                                                                                                                                                                                           STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Segmentation protein cap'n'collar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 MEIRTPDINPAWYASRGIRPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 33, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP001517; BAB06619.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38188 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 45.5
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; D84012; D84012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 AA;
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            Fuji F., Hirar
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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CNC_DROME
        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
     (Membrane sialidase) (Ganglioside sialidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoconjugates. CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                   Miyagi T., Wada T., Iwamatsu A., Hata K., Yoshikawa Y., Tokuyama S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CTT-2003 (Rel. 42, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    벙
                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
f.1.
                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning and characterization of a plasma membrane-associated sialidase specific for gangliosides.";
J. Biol. Chem. 274:5004-5011(1999).
-!- FUNCTION: Plays a role in modulating the ganglioside content the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50; DB 1; Length 428;
Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418B34F3245A8F21 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BNR 1.
BNR 2.
BNR 3.
FRIP MOTIF.
By similarity.
Potential.
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By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, ABG08184; BAA75071.1; -.
InterPro; IPR002860; GH_BNR.
Pfam; PF20212; BNR; 3:
Hydrolase; Glycosidase; Membrane; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RARPHSLMIYSDDLGATWHHGRLIKPM 221
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Potential
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                                                                                                                                                                                                                                                                                                MEDLINE=99143165; PubMed=9988745;
  Sialidase 3 (EC 3.2.1.18) (Membr
(N-acetyl-alpha-neuraminidase 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 30.1%;
Local Similarity 33.3%;
es 9; Conservative
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20140
20140
2017
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ARGC BACHD
ID ARGC BACHD
AC Q9K8V7;
DT 28-FEB-2003 (
DT 28-FEB-2003 (
DT 10-OCT-2003 (
DT N-acetyl-gamm
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Gaps

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SITE ACT SITE ACT SITE ACT SITE ACT SITE

REPEAT REPEAT REPEAT

ACT_SITE SEQUENCE

SITE

ACT

Query Match

Matches

8 g

195 N

Length 345; Indels

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10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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TRANSFAG; T01998; ...
DR FlyBase; FBGN0000338; cnc.
DR GG; GG:0003634; Cnucleus; IDA.
DR GG; GG:0003637; F:DNA binding; IMP.
GG; GG:000367; F:DNA binding; IMP.
GG; GG:0007350; P:Dlastoderm segmentation; IMP.
DR GG; GG:0007310; P:cocyte microtubule cytoskeleton polarization; IMP.
DR GG; GG:00042070; P:cocyte microtubule cytoskeleton polarization; IMP.
DR GG; GG:000359; P:regulation of bicoid mRNA localization; IMP.
DR GG; GG:0007317; P:regulation of pole plasm oskar mRNA localiz. ..; IMP.
DR InterPro; IPRO04827; TF_BZIP.
DR INTERPRO; IRRO4827; TF_BZIP.
DR SWART; SMG0338; BRLZ; 1.
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB. outstation the Lucopean Bioinformatics Institute. There are or estrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
FUNCTION: Plays a role in cephalic patterning. Probable subunit of a heterodimeric regulatory protein involved in the control of head morphogenesis.

DEVELOPMENTAL STAGE: Localized to the mandibular segment and the hypopharyngeal and labral primordia first detectable in late
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ∑ ω
:
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50217; BZIP, 1.
PROSITE; PS00036; BZIP BASIC; 1.
Transcription regulation; Activator; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins |
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
XSEA OR SCO5056 OR SCK7.29C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.6%; Score 47.5; DB 1; Length 533; 37.5%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                              blastoderm stages.
SIMILARITY: Belongs to the bZIP family. CNC subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB59246).
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> L (IN REF. 1;
EADFF9A5D6CA5C5F
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASIC MOTIF.
LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||| ::| |: || ::
HRHVFQYLRDPEGNPCWPADYSLQ 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 HRHSME-IRTPDINPAWYASRGIR 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56948 MW;
                                                                                                                                                                                                    EMBL; M37495; AAB59246.1; -.
HSSP; P34707; 1SKN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
'Loc 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Developmental
DNA BIND 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EX7L STRCO
Q9FBM3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                     Nature 417:141-147 (2002).

-!- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligomucleotides, which are then degraded further into small acid-soluble oligomucleotides (By similarity).

-!- CTAINTIC ACTUUTY: Exomucleolytic cleavage in either 5 · to 3 · or 3 · to 5 · direction to yield mucleoside 5 · phosphates.

-!- SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TOWD J. P., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J. F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Fleischmann R.D., Ketchum K.A., Klank H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fulji C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                 Taylor K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) (1-AGP acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
Oliver K., O'Neil S.,
                                                                                                                                                              Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ю
Э
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil
Rabbinowitsch E., Rajandream M.A., Ruthbríord K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares R., Tayl
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL939122; CAC05901.1; -.

HAMAP; MF_00378; -; 1.

InterPro; IPR004375; Exonuc_VII_L.

InterPro; IPR004365; TRNA_anti.

Pfam; PF02601; Exonuc_VII_L; 1.

Pfam; PF01336; TRNA_anti; 1.

TIGRPAMs; TIGR00237; XsSA; 1.

Hydrolase; Nuclease; Exonuclease; Complete proteome.

SEQUENCE 402 AA; 43882 MW; 145929A8372B4E08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.3%; Score 47; DB 1; 47.6%; Pred. No. 18; ive 1; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEWYAPRGOLSLRAABIKPVG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 PAWYASRG-----IRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
                                                                                                                                                                                                                                                coelicolor A3(2)
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Query Match
Best Local Similarity 34.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=198094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE
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Q81JW1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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STATE THE STATE OF THE STATE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausber R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buttow K.H., Schemer C.F., Bhat N.K.,
A Diatchento L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Diatchento L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
B, Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                    Nature 188:539-547(1997).

Nature 188:539-547(1997).

Nature 188:539-547(1997).

Nature 2 position: Converts lysphosphatidic acid by incorporating acyl moiety at the 2 position.

Natural Acrivity: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate = CCA + 1,2-diacyl-sn-glycerol 3-phosphate.

Natural De novo phospholipid biosynthesis; second step.

NATHWAY: De novo phospholipid biosynthesis; second step.

NATHWAY: Belongs to the 1-acyl-sn-glycerol-3-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
NAD-dependent deacetylase sirtuin 4 (EC 3.5.1.-) (SIR2-like protein
"The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IRR00123; Acyltransferase.
InterPro; IRR004552; AGP acyltrn.
Pfam; PP01553; Acyltransferase; 1.
SWAR; SWO653; Plsc; 1.
IGRPAMs; TIGR00530; AGP acyltrn; 1.
Phospholipid biosynthesis; Transferase; Acyltransferase;
Inner membrane; Complete proteome.
SEQUENCE 240 AA; 27745 MW; 22BD5D0EB190BBDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.0%; Score 46.5; D
47.6%; Pred. No. 12;
iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 ARTRIVMLESYTPDFNSPTWY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRIHRHSMEIRIPDIN-PAWY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IS-WAR-2004 (Rel. 43, Created)
IS-WAR-2004 (Rel. 43, Last seq.
IS-WAR-2004 (Rel. 43, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000636; AAD08393.1; -. PIR; D64688; D64688.
                                                                                                                                                                                                                                              acyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HP1348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIR4 MOUSE
Q8R216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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d
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Mara M.A., Schein J.E., Jones S.J.M., Mara M.A., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        closely related bacteria.";
Nature 423:81-86(2003).
-!- FUNCTION: Catalyzes the ATP-dependent amination of UTP to CTP with
                                                                                                                                                     and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S. Debendent deacetylase (By similarity).

-!- FUNCTION: Probable NAD(+) + an acetylprotein = nicotinamide + O-

-!- CATALYTIC ACTIVITY: NAD(+) + an acetylprotein = nicotinamide + O-

-!- CATALYTIC ACTIVITY: Deform to the sirtuin family.

-!- SIMILARITY: Belongs to the sirtuin family.

-!- SIMILARITY: Contains 1 deacetylase sirtuin-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-WAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CTP synthase (RC 6.3 4.2) (UTP--ammonia ligase) (CTP synthetase)
PYRG OR CTRA OR BA5583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
; 199FBF199617DBCO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIRTUIN-TYPE.
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 18;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RTHRHSMEIRTPDINPAWYA-SRGIRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, BC022653; AAH226531; ALT INIT.
MGD, MGD; MGD; A910596017Rik.
InterPro; IPR003000; SIR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF02146; SIR2; 1.
PROSITE; PS50305; SIRTUIN; 1.
Hydrolase; NAD; Metal-binding; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22608414; PubMed=12721629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37555 MW;
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34.5%;
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European Bioinformatics Institute.
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                                                                                   A40778; MINWINE.
                                                                                             , C41.001;
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                                                                                                                                                                                                                                                                                                                                                         Matches
Вb
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                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
         similarity).
-!- CATALYTIC ATTP + UTP + NH(3) = ADP + phosphate + CTP.
-!- ENZYME REGULATION: Allosterically activated by GTP, when glutamine is the substrate. Inhibited by CTP (By similarity).
-!- PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP; third
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: HEPATITIS E VIRUS IS THE MAJOR CAUSATIVE AGENT OF ENTERICALLY TRANSMITTED NON-A, NON-B HEPATITIS (ET-NANBH).
                                                                               -i- SUBUNIT: Homotetramer (By similarity).
-i- SIMILARITY: Belongs to the CTP synthase family.
-i- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-10903 (Rel. 41, Last annotation update)
Non-structural polyprotein [Contains: RNA-directed RNA polymerase (EC 2.7.7,48); Helicase].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length viral genome.",
Virology 185:120-131(1991).
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing of the
L-glutamine or ammonia as the source of nitrogen (By
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ش
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEDLINE=92024067; PubMed=1926770; MEDLINE=92024067; PubMed=1926770; Tram A.W., Smith M.W., Guerra M.E., Huang C.-C., Bradley D.W., Fry K.E., Reyes G.R.; Mepatitis E virus (HEV): molecular cloning and sequencing of
                                                                                                                                                                                                                                                                                                     TIGREAMS; TIGR00337, PyrG, 1.
PROSITE; PS00442; GATASE TYPE I; 1.
Pyrimidine biosynthesis; Ligase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 535;
                                                                                                                                                                                                                                                                                                                                                     AMINATOR DOWAIN.
GLUTAMINE AMIDOTRANSFERASE.
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
GATASE (BY SIMILARITY).
A, 05FC670F9D77AB97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses, ssRNA positive-strand viruses, no DNA stage,
Hepatitis E-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46.5; DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 HRHSMEIRT---PDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis E virus (strain Burma) (HEV).
                                                                                                                                                                                                                                             TIGR; BA5583; -.
HAMAR; MF 01227; -; 1.
InterPro; IPR000991; GATase_1.
InterPro; IPR004468; PyrG_synth.
Pfam; PF00117; GATase; 1.
                                                                                                                                                                                                                                EMBL; AE017041; AAP29225.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   59752 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           28.0%;
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535
381
507
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381
507
509
535 AA;
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DOMAIN 1
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                                                                      (last) step.
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Best Local Simi
Matches 11;
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SEQUENCE
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                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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   restrictions on
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MEDLINE=3327573; PubMed=8470371;
Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Ichikawa M.,
Rikihisa T., Winn K.;
"Sequence and gene structure of the hepatitis E virus isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virus Genes 7:95-109(1993).
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-00T-1993 (Rel. 27, Created)
01-00T-1993 (Rel. 27, Last sequence update)
01-00T-1993 (Rel. 41, Last sequence update)
Non-structural polyprotein [Contains: RNA-directed RNA polymerase (EC 2.7.7.48); Helicase].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01661; Alpp; 1. Pfam; PF0341; Peptidase C41; 1. Pfam; PF03478; RNA dep RNAD12; 1. Pfam; PF01443; Virāl helicase; 1. Pfam; PF01649; Vmethyltransf; 1. SMART; SM00506; Alpp; 1. Polyprotein; Transferase; RNA-directed RNA polymerase; Helicase; Polyprotein; Transferase; RNA-directed RNA polymerase; Helicase; RTP-binding 975 SE2 ATP (POTENHIAL); SEQUENCE 1693 AA; 185191 MW; 2P355E46E9ED219B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis E virus (strain Myanmar) (HEV), Viruses, ssRNA positive-strand viruses, no DNA stage; NGBLILSE-like viruses.
There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; DB 1;
1e+02;
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Pred. No. 1e+02
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1693 AA
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                                                                                                                                                                                                                                                                          InterPro; IPR002589; Alpp.
InterPro; IPR00188; Peptidase C41.
InterPro; IPR001788; RNA dep KNApol2.
InterPro; IPR007094; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_Psvir.
InterPro; IPR007094; RNA_pol_Psvir.
InterPro; IPR002588; V_methyltransf.
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37.0%;
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nes 10; Conservative
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  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canaani E.; .
"Structure and expression pattern of human ALR, a novel gene with
strong homology to ALL-1 involved in acute leukemia and to Drosophila
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22371496; PubMed=1,
Goo Y.-H., Sohn Y.C., Kim D.-H., Kim S.-W., Kang M.-J., Jung D.-J.,
Kwak E., Barlev N.A., Berger S.L., Chow V.T., Roeder R.G.,
Azorsa D.O., Meltzer P.S., Suh P.-G., Song E.J., Lee K.-J., Lee Y.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee U.W.;
"Activating signal cointegrator 2 belongs to a novel steady-state
"Activating signal cointegrator 2 trithorax group proteins.";
Mol. Cell. Biol. 23:140-149(2003)
-!- FUNCTION: May be involved in transcriptional regulation.
-!- FUNCTION: May be involved in transcriptional regulation.
-!- FUNCTION: May be involved in transcriptional regulation.
-!- SUBUNIT: Belongs to the ASC-2/NCOA6 complex (ASCOM), which contains ASC-2/NCOA6, the retinoblastoma-binding protein RBQ-3/RBP5, alpha- and beta-tubulins, the trithorax group proteins mills and MLL3, and ASH2/ASCL2.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                     014686, 014687;
10-007-2003 (Rel. 42, Created)
10-007-2003 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myeloid/lymphoid or mixed-lineage leukemia protein 2 (ALL1-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

BEDLINE-37388494; PubMed-9247308;

Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,

Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                     Polyprotein; Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
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H
                                                                                                                                                                                               Query Match 28.0%; Score 46.5; DB 1; Length 1693; Best Local Similarity 37.0%; Pred. No. 1e+02; Matches 10; Conservative 5; Mismatches 11; Indels 1;
                                                                                                                                                               82 ATP (POTENTIAL).
185215 MW; AAB4C9140A7E21EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=O14686-2; Sequence=VSP_008563, VSP_008559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERACTION WITH ASC-2/NCOA6 CONTAINING COMPLEX.
                                                                                                                                                                                                                                                                                                                               PRT; 5262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=014686-1; Sequence=Displayed;
                                                                                                                                                                                                                                                            InterPro; IPR00178; Peptidase_C41.
InterPro; IPR001789; RNA_Gol_D8_F8.
InterPro; IPR001799; RNA_Gol_D8_F8.
InterPro; IPR007094; RNA_POl_D8_F8.
InterPro; IPR005089; V_methyltransf.
InterPro; IPR005089; V_methyltransf.
Pfam; PP01661; Alpp; 1.
Pfam; PP01661; Alpp; 1.
Pfam; PP01441; Peptidase_C41; 1.
Pfam; PP01443; Viral_helicase1; Pfam; PP01643; Viral_helicase1; 1.
Pfam; PP01660; Wiral_helicase1; 1.
SMART; SM00506; Alpp; 1.
                                                                                                                                                                                                                                               2 RTHRHSMEIRTPDINPAWY-ASRGIRP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 15:549-560(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Cervical carcinoma;
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                                                                                                                                                                  982
                                                                                                                                                                          1693 AA;
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Missing (in isoform 2).
/FTId=VSP 008563.
PMSELPAHSWKCKACRVCRACGAGSAELNPNSEWFENYSLC
                                                                                                                                                                                                 11;
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Pred. No. 3.5e+02;
5; Mismatches 10; Indels 11;
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                                                PRO-RICH.
ARG-RICH.
CYS-RICH.
GLN-RICH.
PRO-RICH.
PRO-RICH.
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PRO-RICH.
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Best Local Similarity 31.6%;
Matches 12; Conservative
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Search completed: August 12, 2004, 14:44:52 Job time : 9.11047 secs

2037 SGTHLGGLELKTPDVFKAPLTPRASQVEPQSPGLGLRP 2074

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

August 12, 2004, 14:37:35 ; Search time 42.7151 Seconds (without alignments) 228.984 Million cell updates/sec

US-09-700-643A-2 166 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRX 31 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:* Database :

sp_organelle:*
sp_phage:*
sp_plant:*
sp_prodent:*
sp_vront:*
sp_vrontebrate:*
sp_vrontebrate:* sp_archea.*
sp_bacteria.*
sp_fungi.*
sp_inwan.*
sp_invertebrate.*
sp_mammal.* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O8wn12 ovis aries	O9w624 carassius a	Q9ilw4 pseudomonas	Q7upg7 rhodopirell	087474 burkholderi	O7vsal bordetella	006348 mycobacteri	Q7twe6 mycobacteri	094ku9 brassica ca	094fz9 brassica ca	Q9a5e9 caulobacter	Q9m371 arabidopsis	026276 methanobact	Q7z6v1 homo sapien	Q9da19 mus musculu	neines amon 783030
ΠD	Q8WN12	O9W624	Q911W4	Q7UPG7	087474	O7VSA1	006348	Q7TWE6	Q94 KU9	Q94FZ9	Q9A5E9	Q9M371	026276	Q7Z6Y1	Q9DA19	060687
DB	9	13	16	16	7	16	16	16	10	10	16	10	17	4	11	4
Query Match Length DB	1 860	117	664	1120	315	314	314	314	327	327	637	790	785	54	450	465
Query	91.6	55.4	34.0	33.7	33.1	32.5	32.2	32.2	31.9	31.9	31.9	31.9	31.3	30.7	30.7	30.7
Score	152	92	56.5	56	22	54	53.5	53.5	53	53	53	53	52	51	51	
Result No.		~	m	4	د	9	7	80	6	10	11	12	13	14	15	5

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1 Q8WW85 2 Q45883 16 P74747 16 Q7WP50 16 Q7W1E3	0000	16 Q8FM04 3 Q08689 16 Q9EYB3 17 Q97A00 16 Q7URC6		16 Q892Q2 16 Q80EW0 16 Q8PERO 16 Q91022 16 Q7WX13 2 Q88002 16 Q45375
123 123 3128 3144 444	625 692 939 1253	1654 176 72 173 187	326 402 663 1245 303 436	8 4 4 4 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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ALIGNMENTS

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Gaps
                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Preproprolactin-releasing peptide.
Ovis aries (Gheep).
Enkaryots, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Curlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T., "Prolactin-releasing peptide (PrRP) in the ewe: CDNA cloning, mRNA distribution and effects on prolactin secretion in vitro and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vivo.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF450453; AAL47178.1; -.
SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAAB5 CRC64;
                                                                                                        98 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 52
                                                                                                        PRT;
                                                                                                        PRELIMINARY;
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                                                                                             Q8WN12
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RESULT 1
Q8WN12
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                                                                                                                                                          A REPARATION OF THE REPARATION
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Created)
Last sequence update)
Last annotation update)

01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,

117 AA.

PRT;

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Q9W624

O9W624 ID 099 AC 099 DT 011

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33.7%;
64.3%;
                                       (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 25,
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Best Local Similarity 64...
9; Conservative
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                                                                                                                                                  Rhodopirellula baltica.
                                                                                                        Hypothetical protein.
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                                         01-OCT-2003
01-OCT-2003
01-OCT-2003
Q7UPG7
Q7UPG7;
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STRAIN=ATC (1562 / PAO1;
STRAIN=ATC (1562 / PAO1;
STRAIN=ATC (1562 / PAO1;
Stover C.K., Pham X.Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.G., Brinkman F.S.L., Hufnagle W.G., Kowalla, D.G., Lagrou M.,
Hickey M.G., Brinkman F.S.L., Hufnagle W.G., Kowalla, D.G., Lagrou M.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulzen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                          Gaps
             Carassius auratus (Goldfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                         / Match 55.4%; Score 92; DB 13; Length 117; Local Similarity 52.0%; Pred. No. 1.1e-05; les 13; Conservative 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                            Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide)";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 FW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypotherical protein, Complete proteome.
SEQUENCE 664 AA, 76329 MW, 8F59FEED54C308AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PA2151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       opportunistic pathogen.";
Nature 406:959-964(2000).
Nature 406:959-964(2000).
EMBL, AE004642, AAG05539.1; -.
PIR, F83376; P83376.
GO; GO:0003779; F:actin binding; IEA.
GO; GO:0004556; F:actin binding; IEA.
GO; GO:0005975; P:actin binding; IEA.
InterPro; IPR001589; Actbind_actin.
InterPro; IPR006047; Alpha amyl_cat.
Pfam; PF00128; alpha amylase; I.
PROSITE; PS00019; ACTININ_1; 1.
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45.8%; Pred. No. 12;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      6 HSMEIRTPDINPAWYASRGIRPVGR 30
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                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=287;
                                                                                                                                                                           TISSUE-Brain;
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Q911W4;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22735913; PubMed=12835416; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Gloeckner F.O., Kube M., Bauer M., Heitmann K., Rabus R., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99121037;
MEDLINE=99121037;
Haigler B. E., Johnson G.R., Suen W.C., Spain J.C.;
Haigler and genetic evidence for meta-ring cleavage of 2,4,5-
Embl. Aboroxytoluene in Burkholderia sp. strain DNT.";
J. Bacteriol. 181:965-972(1999).
EMBL, AF076848; AAD12738.1;
PITTERPOY. IPR0049360; Gly_Dale_diox.
Pfam; PF00903; Glyoxalase; 1.
Pfam; PF00903; Glyoxalase; 1.
SEQUENCE 315 AA; 34745 MW; E99261179022961E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                 Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pireliula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 16; Length 1120;
Pred. No. 24;
3; Mismatches 2; Indels (
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33.1%; Score 55; DB 2; Length 315;
Best Local Similarity 44.4%; Pred. No. 8.7;
Matches 16; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL, BX294145; CAD75095.1; -
Hypothetical protein; Complete protecme.
SEQUENCE 1120 AA; 123221 MW; 67C757873421BF9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                            Last sequence update)
Last annotation update)
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Created)
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MEDLINE=93194809; PubMed=8449889;
Suen W.C., Spain J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2,4-dinitrotoluene degradation.";
J. Bacteriol, 175:1831-1837(1993)
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1 SRTHRHSMEIRTPD---INPAWYASRGIRP---VGR 30

RESULT 4 Q7UPG7

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SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nalson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                               laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                 "Whole genome comparison of Mycobacterium tuberculosis clinical and
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00106; adh short; 1.
PROSTIE; P800061; ÄDH SHORY; 1.
Hypothetical protein; Oxidoxeductase; Complete proteome.
SEQUENCE 314 AA, 33194 MW; 26144BA917E09274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.2%; Score 53.5; DB 16; 27.5%; Pred. No. 14; rative 5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                 activity; IEA.
                                                                                                                                                                                                                                                           EMBL, 295390, CAB08708.1, -.
EMBL, AE07162, AAK47948.1; ALT_INIT.
PIR, B70569, B70569.
THSP, P21132; 1DFI.
TIGR, MT3589; --
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                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016491; F:oxidoreductase a GO; GO:0008152; P:metabolism; IEA. InterPro; IPR002198; ADH short.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 27.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                   complete genome sequence.
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                   Tuberculist; Rv3485c; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SRTHR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                  (SDR) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q7TWE6
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                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN=Tobama I / ATCC BAA-589 / NCTC 13251;

MATAIN=Tobama I / ATCC BAA-589 / NCTC 13251;

MEDLINE=228254; PubMed=12910271;

A Parkhil J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

A Harris D.E., Holden M.TG., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cromin A., Davis P., Doggett J.,

Chillingworth T., Collins M., Cromin A., Davis P., Doggett J.,

Leather S., Moubercak H., O'Neil S., Ormond D., Frice C.,

Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Nowin L., Whitehead S., Barrell B.G., Maskell D.J.;

Comparative analysis of the genome sequences of Bordetella pertussis,

Nat. Genet. 35:32-40(2003).

REMBL, BKG4012; CAR448661;

REMBL, BKG4012; CAR448661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Biglmeier K., Gas S., Barry C.E. Ill, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
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0
                                                                                                                                                                                                                            Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.5%; Score 54; DB 16; Length 314; 54.5%; Pred. No. 12; cive 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Oxidoreductase, short-chain
dehydrogenase/reductase family)
RV3485C OR MT3589 OR MTCX13E12.38C.
Mycobacterium tuberculosis.
                                                                                                                                                     Last sequence update)
Last annotation update)
216 SRMHHGSFEIQDLDAQFIGNKWLASRGWKPGWGVGR 251
                                                                                                                                                   update)
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                                                                                                    314 AA
                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 SMEIRTPDINPAWYASRGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98295987; PubMed=9634230;
                                                                                                                                  (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                    PRELIMINARY;
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                                                                                                                                                                              Arginase (EC 3.5.3.1)
BP0538.
                                                                                                                                                                                                                      Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
STRAIN=H37Rv;
                                                                                                                                  01-OCT-2003 (
01-OCT-2003 (
01-OCT-2003 (
                                                                                                                     DAVSA1;
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                                                                                                    Q7VSA1
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                                                                                    07VSA1
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Length 314;

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Gaps
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EMBL. BX48346; CAD95701.1; -
Oxidoreductase; Complete proteome.

Oxidoreductase; Complete proteome.
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1765,
                                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable short-chain type dehydrogenase/reductase (EC 1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 SNTHRWFGAYGVTKSAVDHMMKLAADELGPSWVRVNSIRP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                 27
                                                                                  ---HSMEIRTPDINPAWYASRGIRP
                                                                                                                                                                                                                                     314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.2%; Score 53.5; D. 27.5%; Pred. No. 14; ive 5; Mismatches
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Q94KU9

99,4 KU9 99,9 PP 101,10 PP

RESULT 9

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CC2501.
Caulobacter crescentus.
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSS0110; RESPONSE REGULATORY, 1.
Kinase; Phosphorylation; Sensory transduction; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637 AA; 68511 MW; OEDEEAF76FFA8611 CRC64;
                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JCT-2003 (TrEMBLrel. 25, Last annotation update)
Sensory box histidine kinase/response regulator.
                      637 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0344; BCTRISENSOR.
Prodon; PRO000039; Response reg; 1.
SMART; SM00387; HATPASAS C; 1.
SMART; SM00388; HisKA; I.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAC; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sensory_box; 1.
                      PRT;
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                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO0229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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SEQUENCE 637 AA;
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                      Q9A5E9,
Q9A5E9;
Q9A5E9
                           NAMES OF THE PROPERTY OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eddicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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MEDLINE=21249173; PubMed=11351096;

Kim H.U., Wu S.S., Ratnayake C., Huang A.H.;

Kim H.U., Wu S.S., Ratnayake C., Huang A.H.;

Brassica rapa Has Three Genes That Encode Proteins Associated with

Different Neutral Libids in Plastids of Specific Tissues.";

Plant Physiol. 126:330-341(2001).

EMBL, AF200566; AAS57564.1;

EMBL, AF20005198; F.structural molecule activity; IEA.

InterPro; IPRO06843; PAP fibrillin.

Pfam, PF04755; PAP fibrillin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Min. M. W. S. C. Rathadrake C., Huang A.H.;

"Brassica rapa Has Three Genes That Encode Proteins Associated with
Different Neutral Lipids in Plastids of Specific Tissues.";

Plant Physiol. 126:330-341(2001).

EMBL; AP290563; AAK57561.1; -..

GO; GO:0005198; F:structural molecule activity; IBA.

Interpro; IPR006843; PAP fibrillin.

PÉam; PR04755; PAP fibrillin; 1.

SEQUENCE 327 AA; 35678 MW; 8C7B87FCD6C02422 CRC64;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.9%; Score 53; DB 10; Length 327; 43.8%; Pred. No. 18;
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                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Plastid-lipid associated protein PAP1.

Brassica campesris (Field mustard).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Plastid-lipid associated protein PAP1.
Brassica campestris (Field mustard).
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                                                                                         327 AA
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                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=21249173; PubMed=11351096;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 HRHSMEIRTPDINPAW 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 43.8
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 43.8
les 7; Conservative
                                                                                    PRELIMINARY;
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45

Q94FZ9,

RESULT 10

Query Match

Matches

8 엄

Gaps .. 0 31.9%; Score 53; DB 16; Length 637; 48.0%; Pred. No. 36; 6 4; Mismatches Conservative 12; Matches

Query Match

Best Loca Matches

ò 쇰 RESULT 11

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GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:000155; F:two-component sensor molecule activity; IEA.
GO; GO:000156; F:two-component sensor molecule activity; IEA.
GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
InterPro; IRR003594; APPbind ArPase.
InterPro; IRR00515; BPD transp.
InterPro; IRR005467; His_kinase.
InterPro; IRR000460; PAS-assoc_C.
InterPro; IRR000014; PAS-assoc_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawlor S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035608; CAB55682.1; -.
NON TER 54 54 54
SEQÜENCE 54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   785 AA; 87726 MW; ADD502C928307986 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
DJ479917.3.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                       ## PROSITE; PROGRAM:

## PERSON PROGRAM:

## P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 52; DB 1; Pred. No. 64; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412 HRATFRIRRPDGNYRWVEYVDRPIRTDG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 HRHSMEIRTPDINPAW--YASRGIRPVG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.7%;
50.0%;
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01-JUN-2001 (TrEMBLrel. 1'
01-OCT-2003 (TrEMBLrel. 2'
1700023B02Rik protein.
CIR OR 1700023B02RIK.
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hes 13; Conservative
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CATALINE-Belta H.

CATALINE-BO1514; PubMed=9371463;

MEDLINE=98037514; PubMed=9371463;

MIDLINE=98037514; PubMed=9371463;

Andredge T., Bachirzadch R., Blakely D., Cook K., Gilbert K.,

Andredge T., Bachirzadch R., Blakely D., Cook K.,

Andredge T., Bachirzadch R., Blakely D., Cook K.,

Andredge T., Bachirzadch R., Blakely D., Cook K.,

Andredge T., Bachir R., Wicare R.,

Andredge T., Bachir R., Wargle P., Lumm W., Pothier B., Qiu D.,

Spadafora R., Vicare R., Wang Y., Werzbowski J., Gibson R.,

Andredge T., Bach D., Safer H., Patwell D., Frabhakar S.,

Andredge T., Mac J.-T., Rice P., Noelling J., Reeve J.N.;

Andredge T., Mac J.-T., Rice P., Noelling J., Reeve J.N.;

Andredge T., Mac J.-T., Rice P., Noelling J., Reeve J.N.;

T. Camplete genome sequence of Methanobacterium thermoaucotrophicum

RT Geltah: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

EMBL; AE000805; AAB84680.1; -.

DR RN, Feogogy: Foogog.

RO; GO:00162020; C:membrane; IEA.

RO; GO:00162020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TAXID=3702,
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Best Local Similarity 55.6%; Pred. No. 46; Matches 10; Conservative 2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132559; CAB71097.1; -.
PIR; TA7959; T47959.
Hypothetical protein.
SEQUENCE 790 AA; 87376 MW; B222724B75690F30 CRC64;
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Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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01-JAN-1998 (TrEMBLrel. 05, Last seque
01-OCT-2003 (TrEMBLrel. 25, Last annot
sensory transduction histidine kinase.
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                                                                                   Methanobacterium thermoautotrophicum.
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RC STRAINGSTBL/63, TISSUB=Testis;

MEDLINE=21085660; PubMed=11217851;

A Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arawawa T., Shinagawa A., Shibata K., Yoshino M., Adachi J., Fukuda Y., Arawawa T., Hara A., Erkunishi Y., Konno H., Adachi J., Fukuda S., Arawawa T., Hara A., Erkunishi Y., Kiyosawa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Saito R., Matsuda H.A., Ashburner M., Balalor T., Saito R., Adota K., Matsuda H.A., Gissi C., King B., Kochiwa H., Radota K., Matsubi F., Suzuki R., Tomita M., Wagner L., Washio T., Rashim M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G., Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Hofman M., Hume D.A., Kamiya M., Lee N.H., Loyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoco N., Arachi, R., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whittaker C., Whittaker C., Wilming L., Whitnakw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki.S.,
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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MGD; MGI:1914185; Cir.
GO; GO:0005189; F:electron transporter activity; IEA.
GO; GO:0006118; F:electron transport; IEA.
InterPro; IFR000345; CytC heme BS.
PROSITE; PS00190; CYTOCHRÖME_C; 1.
SEQUENCE 450 AA; 51852 MW; F32F11BE6D6A4EAC CRC64;
                                                                                                                                          SEQUENCE FROM N.A.
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Search completed: August 12, 2004, 14:49:01 Job time : 43.7151 secs

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Best Loca Matches

6; Gaps

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August 12, 2004, 14:37:35; Search time 65.7849 Seconds (without alignments) 133.146 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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166
1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRX 31
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
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4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scription	Aay49299 19P2 liga Aaw31391 Human typ Aaw87651 Human typ Aaw87515 Human typ Aay49291 19P2 liga Aab10362 Human oxy Aab10362 Human Oxy Aac26401 Human PrR Aac26401 Human PrR Abu60843 Peptide p Abu60849 Peptide p Adu60849 Peptide p Aav31329 Human oxy Aag62532 Human oxy Aag62532 Human oxy Aag62532 Human oxy Aag62532 Human typ Aav31390 Human oxy Aag62531 Human cRH Abu60845 Peptide p Aaw31230 Human typ Aab10361 Human oxy Aag62530 Human cRH Abu60845 Peptide p
SUMMARIES	AAY49299 AAW31391 AAW31391 AAW31391 AAW97235 AAY49291 AAB10362 AAB10362 AAW11392 AAW31392 AAW31393 AAG62533 AAW91390 AAW91390 AAW91390
DB	WUUUUWW44N00CCUW400W44
Length	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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RESULT 1 AAY49299 ID AAY	JT 1. 1299 AAY49299 standard, peptide, 30 AA.
42;	AAY49299;
4E	22-FEB-2000 (first entry)
(四:	19P2 ligand peptide fragment.
125	Monoclonal antibody, 19P2 ligand, diagnosis, prolactin secretion, pituitary, regulatory mechanism, central nervous system, pancreatic.
SS	Homo sapiens.
X E E E E	Key Modified-site 30 /note= "C-terminal amide"
Z Z	WO9960112-A1.
X E	25-NOV-1999.
P.F.	20-MAY-1999; 99WO-JP002650.
X K :	21-MAY-1998; 98JP-00140293.
Y E	(TAKE) TAKEDA CHEM IND LID.
ž E	Matsumoto H, Kitada C, Hinuma S;
X K	WPI; 2000-039381/03.
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P.	diseases related to ligand abnormality.
PS	Disclosure; Page 27; 73pp; Japanese.
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88	reaction with the part peptide of the C-terminal of 1992 ligand or its
3 5	he pituitary
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88	AY49290-302 represent peptide fragments of the
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Pred. No. 5.4 Mismatches

100.08; Prr 0;

Conservative

Local Similarity

30:

Matches

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Length 31;
DB 2;
Score 165;
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This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 23 to 53 of the sequence represented in AMM1390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaccutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, clistophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglycelactinaemia, asthma, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, reheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinal pincerebellar degeneration, bone fracture, trauma, atopic dermatitis, spinal pincerebellar degeneration, bone fracture, trauma, atopic dermatitis, spinal pincerebellar degeneration, sassays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein
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pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
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                                                         99.4%; Score 165; DB 3; Length 30; 100.0%; Pred. No. 5.2e-18; ive 0; Mismatches 0; Indels
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96JP-00059419.
96JP-00211805.
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                                                                                                                         30; Conservative
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                                                                                           Best Local Similarity
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Sequence 30 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-1996;
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12-AUG-1996;
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                                                         Query Match
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Kitada
                                                                                                                         Matches
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This is the amino acid sequence of the human pituitary G protein-coupled receptor ligand 19P2L. A method suitable for commercial high-level production of 19P2L comprises expressing the ligand in host cells as a recombinant fusion protein much human basic fibroblast growth factor (see AAV83796-97) that has been modified to include an N-terminal collowed by ammonolysis. 19P2L has prolactin secretion-stimulating and closed in the treatment and prevention of various diseases including: senile senelation of the treatment and prevention of various diseases (e.g. of the treatment and prevention of various diseases (e.g. pick's disease, Huntington's disease), infectious diseases (e.g. pick's disease, Huntington's disease), infectious diseases (e.g. pick's disease, Huntington's disease), infectious diseases (e.g. brain trugs, metal and organic compounds), tumourigenic diseases (e.g. brain trugs, metal and organic compounds), tumourigenic diseases (e.g. brain trugs, metal and organic compounds), thourigenic diseases (e.g. brain trugs, metal and organic diseases (e.g. chronic subarachnoidal heamorrhage, and cher types of dementia, depression, hyperactive child syndrome (microencephalopathy) and disturbance of consciousness. It is also useful for prevention and treatment of diseases associated with prolactin hype pituitary adenoma, breast cancer, infertility, impotence and autoimmune disease (incease (incease), infertility, impotence and autoimmune disease (incease), and seminal vestice (incease), and seminal vestice (incease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease (hypersecretion disorders), and seminal vesicle hypoplasia, osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders). The 1992 polypeptide/amide is also useful as a test reagent for study of the prolactin secretory function or as a lactogogue in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g.
                                                                                                                                                                                                                                                                                                                                         1992 ligand, G protein coupled receptor; pituitary;
prolactin releasing peptide; human; dementia; breast cancer; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing a 19P2 pituitary G protein receptor ligand - by cleavage of fusion protein, useful for preventing and treating dementia, breast cancer, renal failure and autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishimura O;
30
                          SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
1 SRIHRHSMEIRTPDINPAWYASRGIRPVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tanaka Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 35; 56pp; English.
                                                                                                                                                            AAW87615 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98EP-00111725.
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                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-047884/05.
                                                                                                                                                                                                                                                                                                  Human 19P2 ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUN-1998;
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                                                                                                                                                                                                                                                    29-MAR-1999
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Query Match

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Sequence 31

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing typoweatholism. They can by used for promoting lyndrome, euthyroid or hypomecabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin print the promoting prolactin as secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorthea, galactorrhea, acromegaly, chiarifrommer isyndrome, Argonz-del Castilo Syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszospermia. The inhibitory agents can also be used for treating or preventing choricocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal lipidmetabolism or oxytocia
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                                                                                                                                                                                                                                               Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCR; hypoovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitulitary adenomatosis; brain tumour; emenopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Porbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy.
                Gaps
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                Indels
 100.0%; Pred. No. 5.4e-18; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsumoto H;
                                           1 SRIHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                             SRITHRHSMEIRTPDINPAWYASRGIRPVGR
                                                                                                                                                                                                                          Human type ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 159; 241pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujii R,
                                                                                                                                           AAW97235 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97JP-00165437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-JP002765.
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                                                                                                                                                                                                 06-MAY-1999 (first entry)
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinuma S, Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-105614/09.
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-1998;
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                 30;
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                 Matches
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Length 31;

Score 165; DB 2; : Pred. No. 5.4e-18;

99.4%; S

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative sequences ANY49290-302 represent peptide fragments of the 19P2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody, 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic.
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Pred. No. 5.4e-18;
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1 SRIHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                     1 SRIHRHSMEIRTPDINPAWYASRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                              AAY49291 standard; peptide; 31 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-JP002650.
                                                                                                                                                                                                                                                                                                       19P2 ligand peptide fragment
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Best Local Similarity 100.'
Matches 30, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-039381/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
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                                                                                                                                                                                                                                                          22-FEB-2000
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidy) and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptides or 3.50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases

The substance of the present invention be used in the exemplification of the present invention
                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, corticotrophin releasing hormone, CRH, G protein receptor ligand, analgesic, hyperaldosteronism, hypercortisolaemia, hypoadrenocorticism, Addison's disease, adrenal gland hyperfunction; obesity.
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                                                                                                                                                                                   Milner PG, Holmes
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                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 244; 733pp; English.
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                                           99US-0134406P.
99US-0153406P.
99US-0159783P.
17-MAY-2000; 2000WO-US013576.
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Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                   Bridon DP, Ezrin AM,
                                                                                                                                     (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                              WPI; 2001-112059/12.
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                                           17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, terine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                              Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary, medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl, maleimido group, amino, hydroxyl, thiol; hormone, growth factor; neurotransmitter.
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                     Human oxytocin secretion promoting peptide SEQ ID NO: 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Prea. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 62; 72pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kitada C, Hinuma
                                                                                                                                                                                                                                                                                                                                                              98JP-00369585
                                                                                                                                                                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD
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Query Match

Matches

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Gaps ö

DB 4; Length 31; 5.4e-18; thes 0; Indels

99JP-00327900.

18-NOV-1999; 26-SEP-2000;

WO200069900-A2

Synthetic.

AAB90991;

RESULT 7

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23-NOV-2000.

(TAKE) TAKEDA CHEM IND LID.

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Best Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; wakefulness; sleep disorder; prolactin releasing peptide receptor; PrRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea; insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
                                         protein receptor ligand or peptide for controlling corticotropin
                                                                                          The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor Ilgand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypodrenocorticism, Addison's disease (including boredom, nausee, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PrRP) receptor (GFRIO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ening for compounds useful for promoting wakefulness or sleep, and treating sleeping disorders, e.g. insomnia, hypersomnia or sleep a, comprises administering a prolactin releasing peptide agonist or
                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                              Length 31;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                Score 165; DB 4; L
Pred. No. 5.4e-18;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                        1 SRIHRHSMEIRIPDINPAWYASRGIRPVGR
                                                                       Claim 3; Page 73-74; 90pp; Japanese
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                                                                                                                                                                                                                                99.4%; SCO1
100.0%; Pre
tive 0; N
 Hinuma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-2000; 2000US-00560915.
                                                    releasing hormone secretion.
                                                                                                                                                                                                                                                      Conservative
  Matsumoto H,
                                                                                                                                                                                                                                                                                                                                                                                                              Human PrRP-31 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-403931/43.
                     WPI; 2001-355552/37
                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIVELLI O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002037533-A1.
                                                                                                                                                                                                             Sequence 31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticonvulsant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-2002
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                                         of G
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compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. PTRP receptor agonists may be used to treat common disorders which lead to sleepiness, e.g. sleep aposea, narcolepsy, idiopathic hypersomnia and psychogenic hypersomnia. PTRP receptor antagonists are useful for disorder and psychophysiologic insomnia such as adjustment sleep disorder and psychophysiologic insomnia. The present sequence is human PTRP-31 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide production by gene recombination associated peptide #27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide production; low-molecular peptide; KiSS-1; GPR8 ligand;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 165; DB 5; I
Pred. No. 5.4e-18;
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Pred. No. 5.4e-18;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TAKE ) TAKEDA CHEM IND
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les 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene recombination
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31 AA;
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Matches

8

RESULT 11 ABU60827 ID ABU6

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This invention relates to a novel human serine protease precursor polypeptide. Specifically, it refers to a novel type II transmembrane serine protease that participates in the control of hormones produced by the pancreatic gland. As such, it can be used in a screening method for the identification of compounds that are useful for the treatment of diseases where a neurohypophysical hormone participates, such as describes the compounds of this invention as antidiabetic and ophthalmological. This peptide sequence is human peptide 2 related to the human serine protease of the invention.
                             human, serine protease precursor, hormone, neurohypophysical, diabetes, diabetic, ophthalmological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease precursor for developing treatment for diabetes and cataracts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor; ligand binding; pharmaceutical; modulator;
pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7; Length 31;
5.4e-18;
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100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW31392 standard; peptide; 32 AA.
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                                                                                                                                                                                                                                                                                                                                        2002JP-00013849.
2002JP-00298003.
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96JP-00059419.
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96JP-00246573.
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Best Local Similarity 100.
Matches 30, Conservative
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                                                                                                                                                                        WO2003062429-A1.
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                                                                                                                                                                                                                                                                                                                                           23-JAN-2002;
10-OCT-2002;
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                                                                                                                                                                                                                             31-JUL-2003
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18-SEP-1996;
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15-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide production by gene recombination associated peptide #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production; low-molecular peptide; KiSS-1; GPR8 ligand;
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Pred. No. 5.4e-18;
     Indels
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100.0%; Pred. No. ...
0; Mismatches
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Mismatches
                                                        1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                    SRIHRHSMEIRTPDINPAWYASKGIRPVGR 30
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                                                                                                                                                                                                                                                  ABU60827 standard; peptide; 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-2002; 2002WO-JP004735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2001; 2001JP-00147341
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                                                                                                                                                                                                                                                                                                                                                                06-MAY-2003 · (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suenaga M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100. es 30; Conservative
30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-129302/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide production
gene recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2003
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Best Local Si
Matches 30;
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RESULT 12 ADC71228

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EXEXEXE Exervises

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Gaps

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Indels

WPI; 2000-452298/39.

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This sequence represents a peptide fragment from a novel human type
ligand polypeptide corresponding to amino acid residues 23 to 54 of the
sequence represented in AMW31390 and is used in an assay to monitor
ligand binding to the G protein-coupled receptor protein. Pharmaceutical
compositions containing this ligand may be used as a pituitary function
modulator. An entral nervous system modulator or a particaric function
modulator. This ligand could have specific applications as a prophylactic
or therapeutic agent for dementia, depression, hyperkinetic syndrome,
content of consciousness, anxiety syndrome, schizophenia, trauma,
growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia,
hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes,
cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma,
cancer, pancreatitis, spinal injury, transient brain ischaemia epilepsy,
amylotrophic lateral sclerosis, acute myocardial infarction, infertility,
spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis,
csteoporosis and/or oligogalactia. Assays can also be developed to screen
compounds which are capable of altering the binding activity of the
ligand affecting activation of the G protein-coupled receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; coxcaesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                       Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland.
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                                                 Hosoya M, Fujii R, Fukusumi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human oxytocin secretion promoting peptide SEQ ID NO: 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.4%; Score 165; DB 2; I 100.0%; Pred. No. 5.7e-18; tive 0; Mismatches 0;
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                                                 Kawamata Y,
                                                                                                                                                                                                             Claim 2; Page 185; 258pp; English.
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               (TAKE ) TAKEDA CHEM IND LTD
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                                               S, Habata Y,
                                                                                                    WPI; 1997-363672/33.
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nes 30; Conserv
                                                                                                                       N-PSDB; AAV02429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32 AA;
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                                                 Hinuma
Kitada
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliocrating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, corticotrophin releasing hormone, CRH, G protein receptor ligand, analgesic, hyperaldosteronism, hypercortisolaemia, hypoadrenocorticism, Addison's disease, adrenal gland hyperfunction; obesity.
                                                                                                                                    This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weapains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence describes a method of controlling the secretion of
                             Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CRH releasing protein related peptide SEQ ID NO: 33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SRIHRHSMEIRIPDINPAWYASRGIRPVGR
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                                                                                                         Disclosure; Page 62; 72pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsumoto H, Hinuma S;
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26-SEP-2000; 2000JP-00297073.
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Best Local Similarity
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CC loss, and hypotension), adrenal gland hypofunction and obesity. The CC present sequence is a peptide used in the exemplification of the CC invention XX Sequence 32 AA;
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	0; Gaps		
	0;		
Length 32;	0; Indels		
DB 4; .7e-18;	, O s	0	0
99.4%; Score 165; DB 4; Length 32; 100.0%; Pred. No. 5.7e-18;	Matches 30; Conservative 0; Mismatches	1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30	SRITHRHSMEIRIPDINPAWYASRGIRPVGR 30
99.4%;	vative	RTHRHSMEIRTPDINPAWYASRGIRPV(IRTPDINPAWY
imilarity	Conser	SRTHRHSME	SRTHRHSME
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Query Match Best Local Similarity	Matches	λ̈́o	Db

Search completed: August 12, 2004, 14:43:54 Job time : 65.9099 secs

us-09-700-643a-2.rapb

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Sequence 15, Appl Sequence 15, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 41, Appl Sequence 28, Appl Sequence 82, Appl Sequence 84, Appl Sequence 84, Appl Sequence 88, Appl Sequence 26, Appl
                                                                                                             August 12, 2004, 14:49:10 ; Search time 54.7907 Seconds (without alignments) 177.617 Million cell updates/sec
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2: / cgn2_6/ptcdata/2/pubpaa/USO7_NEW_PUB.ppp:*
3: / cgn2_6/ptcdata/2/pubpaa/USO6_NEW_PUB.ppp:*
4: / cgn2_6/ptcdata/2/pubpaa/USO6_NEW_PUB.ppp:*
5: / cgn2_6/ptcdata/2/pubpaa/USO7_NEW_PUB.ppp:*
6: / cgn2_6/ptcdata/2/pubpaa/DCO7_NEW_PUB.ppp:*
7: / cgn2_6/ptcdata/2/pubpaa/USO7_NEW_PUB.ppp:*
8: / cgn2_6/ptcdata/2/pubpaa/USO8_PUBCOMB.ppp:*
10: / cgn2_6/ptcdata/2/pubpaa/USO8_PUBCOMB.ppp:*
11: / cgn2_6/ptcdata/2/pubpaa/USO9_PUBCOMB.ppp:*
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13: / cgn2_6/ptcdata/2/pubpaa/USO9_PUBCOMB.ppp:*
14: / cgn2_6/ptcdata/2/pubpaa/USO9_PUBCOMB.ppp:*
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18: / cgn2_6/ptcdata/2/pubpaa/USO0_PUBCOMB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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166
1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRX 31
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US-10-044-592-40

US-10-044-592-41

US-10-044-592-86

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Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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quence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 1	Sequence	Sequence	Sequence	Seguence		Sequence	Seguence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Seguence	Sequence	
32-161	044-59	044-5	26-77	044-592-	044-59	044-592-9	044-59	044-592-7	32-161-1	196-777-1	0-044-5	-932-161-1	0-044-59	.0-096-777-1	0-044-59	.0-044-592-4	32-1	.0-044-592-	.0-036-777-1	-10-044-592-	-10-044-5	-10-389-647-	-10-108-915-3	-09-820-155	-10-424-599-153	-10-369-493-16	0-424-599-27736	-10-424-599-228	0-301-822-19	
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143	143	143	143	143	143	143	143	128	107	107	103	103	103	103	103	103	66	66	66	88	57	56.5	54	54	23	53	52	51	21	
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ALIGNMENTS

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US-09-32-161-15

1 Genence 15. Application US/0932161

2 Patent No. US2020037533A1

3 GENERAL INCRRATION:

3 APPLICANT: Civelli, Olivier

3 APPLICANT: Civelli, Olivier

3 APPLICANT: Lin, Steven

3 TITLE OF INVENTION: Screening and Therapeutic Methods For

3 TITLE OF INVENTION: Screening and Therapeutic Methods For

3 TITLE OF INVENTION: Screening and Therapeutic Methods For

3 TITLE OF INVENTION: Screening and Therapeutic Methods For

4 TITLE OF INVENTION: Proceeding and Therapeutic Methods For

5 TITLE OF INVENTION: Proceeding and Therapeutic Methods For

6 TITLE OF INVENTION: Proceeding And Sleep

7 CURRENT FILING DATE: 2000-04-28

8 FILE REFERENCE: P.UC 4579

8 FILE REFERENCE: P.UC 4679

9 PAPLICANT: D. UC 096-777-15

9 PAPLICANT: CIVELLI, OLIVIER

9 PAPLICANT: CIVELLI, OLIVIER

9 PAPLICANT: CIVELLI, OLIVIER

9 PAPLICANT: Lin, Steven
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91.6%; Score 152; DB 14; Length 31;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13
LENGTH: 31
TYPE: PRT
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Publication No. US20030171270A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Bos taurus
                                                                                             ; ORGANISM: Bos taurus
US-09-932-161-13
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ORGANISM: Bovine
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  TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR PILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 2000-04-28
SOFTWARE: FastSEQ for Windows Version 4.0
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Bublication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REPERENCE: 2463182P

CURRENT FILIAG DATE: 1090-10-10

PRIOR APPLICATION NUMBER: US 09/403639

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR PILING DATE: 1999-25-10

PRIOR PILING DATE: 1999-04-27

PRIOR PILING DATE: 1999-04-27

PRIOR PILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Sequence 13, Application US/09932161
| Patent No. US20020037533A1
| Patent No. US20020037533A1
| APPLICANT: Civel11, Olivier
| APPLICANT: Civel11, Olivier
| APPLICANT: Civel11, Olivier
| TITLE OF INVENTION: Screening and Therapeutic Methods For
| TITLE OF INVENTION: Promoting Wakefulness and Sleep
| TITLE OF INVENTION: Promoting Wakefulness and Sleep
| TITLE OF INVENTION: Promoting Wakefulness and Sleep
| CURRENT APPLICATION NUMBER: US/09/932,161
| PRIOR APPLICATION NUMBER: US 09/560,915
| PRIOR FILING DATE: 2000-04-28
| NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                 Length 31;
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100.0%; Pred. No. 1.2e-16;
tive 0; Mismatches 0;
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99.4%; Score 165; DB 13;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 30; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 30, Conservative
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CORGANISM: Homo sapiens
US-10-044-592-92
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ORGANISM: Homo Sapien
US-10-096-777-15
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US-09-932-161-13
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SEQ ID NO 92
LENGTH: 87
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                                                              Gaps
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TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
FILE REPERENCE: P-UG 534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/99/560,915
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US-10-044-592-39
is Sequence 39, Application US/10044592
is Sequence 39, Application US/10044592
is Publication No. US20020143152A1
is GENERAL INFORMATION:
is APPLICANT: Hiuma, Shuji
is APPLICANT: Hiuma, Shuji
is TITLE OF INVENTION: Polypeptides, their Production and Use
if TITLE OF INVENTION: Polypeptides, their Production and Use
is PILE REFERENCE: 2463103P
is CURRENT APPLICATION NUMBER: US/10/044,592
is CURRENT FILING DATE: 1999-25-10
is PRIOR FILING DATE: 1999-25-10
is PRIOR FILING DATE: 1999-25-10
is PRIOR FILING DATE: 1999-04-27
is PRIOR FILING DATE: 1999-04-28
is SOFTWARE:
is SOFTWARE:
is SOFTWARE:
is SEQ ID NOS: 96
is ENGTH: 31
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Cuery Maích 91.6%; Score 152; DB 9; Length 31; Best Local Similarity 90.0%; Pred. No. 9.2e-15; Matches 27; Conservative 1; Mismatches 2; Indels
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91.6%; Score 152; DB 13;
Best Local Similarity 90.0%; Pred. No. 9.2e-15;
Matches 27; Conservative 1; Mismatches 2;
                                                                                                                    1 SRIHRHSMEIRTPDINPAWYASRGIRPVGR 30
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SOFTWARE: FastSEQ for Windows Version 4.0
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Gaps
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APPLICANT: Fukusumi, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OP INVENTION: Polypeptides, their Production and Use
FILE REPERENCE: 2453052P
CURRENT APPLICATION NUMBER: US 09/403639
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: UP 9-109974
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 28
LENGTH: 98
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APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REPRENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1998-04-27
PRIOR FLING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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Pred. No. 3.1e-14;
1; Mismatches 2;
    1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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                                                                                                       Sequence 28, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
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Best Local Similarity: 90.0°
Matches 27; Conservative
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Best Local Similarity 90.0
Matches 27; Conservative
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US-10-044-592-38
                                                                                       US-10-044-592-28
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SEQ ID NO 38
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US-10-044-592-82
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                                                                                                                                                                                        Sequence 40, Application US/10044592
; Sequence 40, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463U52P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 09/403639
; PRIOR FILING DATE: 1999-25-10
; PRIOR FILING DATE: 1999-04-27
; PRIOR FILING DATE: 1999-04-27
; PRIOR FILING DATE: 1999-04-27
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 96
; COFT. TO NOS: 96
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Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Fukusumi, Shuji
APPLICANT: Fukusumi, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use;
FILE REPRENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP99/01923
PRIOR APPLICATION NUMBER: PCT/JP99/01923
PRIOR APPLICATION NUMBER: PCT/JP99/01923
PRIOR APPLICATION NUMBER: US 9-108974
PRIOR FILING DATE: 1999-04-28
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                       Indels
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90.0%; Pred. No. 9.2e-15; ative 1; Mismatches 2;
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Pred, No. 9.5e-15;
1; Mismatches 2;
                                                                                              SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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91.6%; Score 152; DE
Best Local Similarity 90.0%; Pred. No. 9.8e
Matches 27; Conservative 1; Mismatches
                                                                1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
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Best Local Similarity 90.0%;
Matches 27; Conservative
Best Local Similarity 90.0 Matches 27; Conservative
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: LENGTH: 32
: TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-40
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LENGTH: 33
TYPE: PRT
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US-10-044-592-88

US-10-044-592-88

Sequence 88, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:
APPLICANT: Fukusumi, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463U32P

CURRENT FLING DATE: 2002-01-10

PRIOR APPLICATION NUMBER: US/10/044,592

CURRENT FLING DATE: 1999-04-25-10

PRIOR PILING DATE: 1999-04-27

PRIOR PELING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-27

PRIOR PELING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE:

CONTWANTER OF SEQ ID NOS: 96
FILE REFERENCE: 2463US2P
CURRENT APPLICATION WINDER: US/10/044,592
CURRENT APPLICATION WINDER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
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Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hikusumi, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use;
FILE REFERENCE: 2463US2P
CURRENT FILING DATE: 2002-01-10
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Pred. No. 3.1e-14;
1; Mismatches 2;
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Pred. No. 3.1e-14;
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PRIOR APPLICATION NUMBER: US 09/403639
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Best Local Similarity 90.0%;
Matches 27; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Bovine US-10-044-592-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-044-592-26
                                                                                                                                                                                                                                                                              SEQ ID NO 86
LENGTH: 98
TYPE: PRT
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LENGTH: 98
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                                                                       APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
APPLICANT: Fukusumi, Shoji
APPLICANT: Fukusumi, Shoji
APPLICANT: Fukusumi, Shoji
FILLE OF INVENTION: Polypeptides, their Production and Use
FILLE REFERENCE: 263052P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: UP 9-109974
PRIOR PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 96
SOCTHWARE:
SEQ ID NO 8-2
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hindma, Shuji
APPLICANT: Hindma, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463U32P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: UP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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Pred. No. 3.1e-14;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 84, Application US/10044592; Publication No. US20020143152A1; GENERAL INFORMATION:
              Sequence 82, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.6%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.03
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           // TYPE: PRT
// ORGANISM: Bovine
US-10-044-592-82
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US-10-044-592-84
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US-10-044-592-84
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LENGTH: 98
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Best Local &
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 Sequence Sequence 3

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US-09-421-208-33
US-08-776-971-11
US-08-776-971-122
US-08-776-971-131
US-08-776-971-131
US-08-776-971-115
US-08-776-971-115
US-09-105-678A-29
US-09-105-678A-29
US-09-105-678A-29
US-09-105-678A-39
US-09-105-678A-37
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US-09-560-915-14
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     TOPOLOGY: Linear
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STATE: M.
COUNTRY:
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                                                                                                                                                                                         August 12, 2004, 14:37:36 ; Search time 17.6628 Seconds (without alignments) 90.609 Million cell updates/sec
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Sequence 32,
Sequence 6, A
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Sequence 31,
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. /cgn2 6/ptodata2/iaa/5B_COMB.pep:*
. /cgn2 6/ptodata2/iaa/6A_COMB.pep:*
. /cgn2 6/ptodata2/iaa/6B_COMB.pep:*
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. /cgn2 6/ptodata2/iaa/PCTUS_COMB.pep:*
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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166
1 SRTHRHSMEIRTPDINPAWYASRGIRPVGRX 31
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US-08-105-678A-43

US-09-421-208-9

US-09-421-208-9

US-09-421-208-13

US-09-105-678A-14

US-09-105-678A-14

US-08-105-678A-14

US-08-105-678A-14

US-08-105-678A-13

US-08-176-971-59

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-09-560-915-13
-09-105-678A-32
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Match Length
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Maximum DB seq
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Sequence 9, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
ITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHWAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                            ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: COLLIN, David G.
REGISTRATION NUMBER: 27,026
REFRENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-523-3400
TELEFAX: 617-523-3400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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BRONSTEIN, ROBERTS & CUSHMAN, LLP

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Sequence 9, Application US/09421208
Patent NO. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHWAN. LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%; Score 165; DB 3; Length 31; 100.0%; Pred. No. 5.4e-18; ive 0; Mismatches 0; Indels
                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: JP 9/34331

FILING DATE: 12-MG-1996

APPLICATION NUMBER: JP 8/59419

FILING DATE: 12-MG-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-MG-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 12-MG-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 11-MR-1996

APPLICATION NUMBER: JP 8/211805

FILING DATE: 18-SEP-1996

ATTONNEY/AGBNT INORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SRIHRHSMEIRIPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
PRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
78-08-776-971-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CONIIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                          130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
       ADDRESSEE: DIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 30, Conservative
                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-421-208-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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Kitada, Chieko
INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
99.4%; Score 165; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.4e-18;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INSURION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BROMSTEIN, ROBERTS & CUSHWAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elem PC compatible
COPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: US/09/105,678A
FILING DATE: 27-JUN-1997
ATPONENT/AGENT INFORMATION:
NAME: COLLIN, David G.
REGISTRATION NUMBER: 27,026
REJERENCE/DOCKET NUMBER: 27,026
REJERENCE/DOCKET
SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRIHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                      Sequence 43, Application US/09105678A
Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 61, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYF
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       Suenaga, Masato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 amino acids
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MOLECULE TYPE: peptide
US-09-105-678A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: DIK
STREET: 130 Wa
CITY: Boston
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                                                                                                                                                              US-09-105-678A-43
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US-08-776-971-61
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Sequence 15, Application US/09560915
Patent No. 6383764
Fatent Calvelli, Olivier
FAPLICANT: Lin, Steven
FITLE OF INVENTION: Therapeutic Compositions and Methods
FILE REFERENCE: P-UC 3534
FOURERT PAPLICATION NUMBER: US/09/560,915
FURE REFERENCE: 2000-04-28
FURBER PAPLICANION NAMBER: 2000-04-28
FURBER PAPLICANION NOS: 24
FATENCE FATENCE FOR Windows Version 4.0
FATENCE FAT
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; Sequence 44, Application US/09105678A
; Patent NO. 6103882
; GANERAL INFORMATION:
; APPLICANT: Suenda, Masato
APPLICANT: Mariva, Takeo
; APPLICANT: Nathuara, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIEE, BRONSTEIN, ROBERTS & CUSHWAN, LLP
STREET: 130 Water Street
CITY: Boston
CTUT: Boston
STATE: MA
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.4%; Score 165; DB 4; Length 31; 100.0%; Pred. No. 5.4e-18; ive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
                                                                                                                                                                                                                                                                                                                               Query Match 99.4%; Score 165; DB 3; I Best Local Similarity 100.0%; Pred. No. 5.4e-18; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SRIHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR
                                                                                         | LENGTH: 31 amino acids
| TYPE: amino acid
| STRANDEDNESS:
| TOPOLOGY: linear
| MOLECULE TYPE: peptide
| US-09-421-208-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30; Conservative
      TELEFAX: 617-523-6440
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 31 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Homo Sapien
US-09-560-915-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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US-09-105-678A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-560-915-15
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Sequence 43. Application US/09421208

Patent No. 6256561

GENERAL INFORMATION:

APPLICANT: Suenaga, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Tanaka, Yoko

APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19F2 LIGAND
NUMBER OF SEQUENCES: 52

CORRESPONDENCES: 52

CORRESPONDENCES: 100

STREET: 130 Water Street

CITY: Boston

STREET: 130 Water Street

CITY: Boston

STREET: 130 Water Street

COUNTY: USA

COUNTY: USA

COUNTY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER SAPABLE FORM:

MEDIUM TYPE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: US 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/PAGENT INFORMATION:

NAME: CONILIN PAYA!

PILING DATE: 27-JUN-1997

ATTORNEY/PAGENT INFORMATION:

NAME: CONILIN PAYA!

NAME: CONILIN PAYA!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 165; DB 3; Length 31; 100.0%; Pred. No. 5.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1997
ATIONED APPLICATION NUMBER: US 172118/1997
FILING DATE: 27-JUN-1997
ATIONEY/AGENT INFORMATION:
NAME: CON111, DAVIG G.
APPERENCE/DOCKET NUMBER: 27,026
REFISHATION NUMBER: 27,026
REFISHATION NUMBER: 27,026
REFISHANTION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
TELEPHONE: 31 anino acids
TYPE: ANINO ACID NO: 9:
SEQUENCE CHARACTER:STICS:
LENGTH: 31 amino acids
TYPE: ANINO ACID NO: 9:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SRIHRHSMEIRIPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-09-421-208-43
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Gaps
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Patent No. 625851

GENERAL INCORNATION:
APPLICANT: Moriya, Takeo

APPLICANT: Analas, Yoko

APPLICANT: Analas, Yoko

APPLICANT: Analas, Yoko

APPLICANT: Alshimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
ADDRESSER: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                        Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 32;
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                        Query Match 99.4%; Score 165; DB 3; I
Best Local Similarity 100.0%; Pred. No. 5.6e-18;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.4%; Score 165; DB 3; 100.0%; Pred. No. 5.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SRIHRHSMEIRIPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 09/105,678
FILING DATE: Z6-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: Z7-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGIERRATION NUMBER: Z7,026
REFERENCE/DOCKET NUMBER: Z7,026
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 32 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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STREET: 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MA
COUNTRY: US!
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                               US-08-776-971-62
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CIIY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.4%; Score 165; DB 3; Length 32; 100.0%; Pred. No. 5.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
CORRENT SYSTEM: DOS
SOFTWARE: FASSERG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: O6-Feb-1997
CLASSIFICATION ATMINER: APPLICATION DATA:
APPLICATION NUMBER: OCT/UP96/03821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SRIHRHSMEIRIPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 28-DEC-1996
APPLICATION NUMBER: #P 7/34331
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: #P 8/5919
FILING DATE: 12-MAR-1996
APPLICATION NUMBER: #P 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: #P 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 62, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                      TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          LENGTH: 32 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-105-678A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
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us-09-700-643a-2.rai

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Gaps
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TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-41-208-45

Sequence 45, Application US/09421208

Sequence 45, Application US/09421208

Batent No. 625851

GENERAL INFORMATION:

APPLICANT: Suchaga, Masato

APPLICANT: Tanaka, Yoko

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESSS:

ADDRESSEE: DIEK, BRONSTEIN, ROBERTS & CHOMMATER: 130 Water Street

CITY: Boston

STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
99.4%; Score 165; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8e-18;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                 COMPUTER READABLE FORM:

MUDIUM TYPE: Diskette
COMPUTER: IBM comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
PRIOR DATE: 06-Feb-197
CLASSIFICATION NUMBER: US/08/776,971B
FILING DATE: 26-DE-1997
PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DF 9743371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 18-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 18-PR-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: DAVID 6.
AMME: CONLIN, DAVID 6.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                 Gaps
                                                RESULT 10

US-09-105-678A-45

i Sequence 45, Application US/09105678A

j Patent No. 6103882

APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Toko
APPLICANT: Moriya, Yoko
APPLICANT: Moriya, Yoko
APPLICANT: Moriya, Yoko
APPLICANT: Moriya, Yoko
APPLICANT: Mishimura, Osamu
TITHE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
MUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: ACCOUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/109/105/678A
FILING DATE: 27-JUN-1997
ATOMEY/AGENT INFORMATION:
NAME: COMIN: DAVIA G
REFERENCE/DOCKET NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
99.4%; Score 165; DB 3; I
Best Local Similarity 100.0%; Pred. No. 5.8e-18;
Matches 30; Conservative 0; Mismatches 0;
               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SRTHRHSWEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SRIHRHSMEIRIPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 63, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
Habarta, Yugo
Rawamata, Yuji
Hosoya, Masaki
Fuji, Ryo
Fukusumi, Shoji
Kitada, Clieko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-776-971-63
                 30;
                 Matches
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Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 165; DB 3; Length 87; 100.0%; Pred. No. 1.8e-17; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/JP96/03821
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
FILING DATE: 28-DEC-1995

PULING DATE: 15-MAR-1996

FILING DATE: 15-MAR-1996

APPLICATION NUMBER: JP 8/2911805

FILING DATE: 12-MAR-1996

FILING DATE: 12-MAG-1996

APPLICATION NUMBER: JP 8/246573

FILING DATE: 18-SEP-1996

ATTORNEY/AGRIT INFORMATION:
NAME: CONJIN, DAVIG G.

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REGISTRATION INFORMATION:
TELEPHONE: 617-523-3400

INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SRTHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 SRTHRHSMEIRIPDINPAWYASRGIRPVGR 52
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 59: US-08-776-971-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 135, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 87 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-776-971-135
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KITALE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.4%; Score 165; DB 3; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8e-18;
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APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: «Unknown:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/0796/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 7/343371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRITHRHSMEIRIPDINPAWYASRGIRPVGR 30
                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 26-UN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59, Application US/08776971B Patent No. 6228984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawamata, Yuji
Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-776-971-59
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APPLICANT: HINDER, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Pujii, Ryo
Pukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

99.4%; Score 165; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: «UNKNOWN»

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/2165
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 10-SEP-1996
ATTORNEY/AGGET INFORMATION:
NAME: COMJIA, DAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 47176
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
REQUENCE CHARACTERISTICS:
LENGTH: 87 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SRIHRHSMEIRTPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 SRIHRHSMEIRIPDINPAWYASRGIRPVGR 52
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 135:
US-08-776-971-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 138, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Disket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-776-971-138
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| REFERENCE/DOCKET NUMBER: 47176
| TELECOMMUNICATION INFORMATION:
| TELECOMMUNICATION INFORMATION:
| TELECOMMUNICATION INFORMATION:
| TELEFORM: 617-523-6440
| TELEFAX: 617-52
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us-09-700-643a-3.rpr

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August 12, 2004, 14:37:36; Search time 13.6977 Seconds (without alignments) 217.697 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                          US-09-700-643A-3
169
1 SRAHQHSMETRIPDINPAWYTGRGIRPVGRX 31
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                              Run on:
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283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: Dirl:*
2: Dirl:*
3: Dir2:*
4: Dir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	olact	Mg protoporphyrin	probable magnesium		hyl	_	8	hypothetical prote		_		lease	trar	probable transport	ical	ical	岩		protoporphyrin IX	magnesium-protopor	protoporphyrin IX	Н			protoporphyrin IX	protoporphyrin IX	ata	cal prot	-sulf
		04	62	10	70	16	93	75	50	48	87	57	73	19	04	55	92	71	58	29	51	00	10	21	88	89	$^{\circ}$	m	0
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hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	hypothetical prote	probable aldC prot	beta-glucosidase h	beta-glucosidase h	ARP1 protein - yea	N-ras upstream pro	magnesium-protopor	TNF receptor assoc	probable gcvB prot	ferripyochelin-bin	probable oxidoredu	conserved hypothet
F84587	F83376	AC3169	A81811	AH3166	D70885	T09021	T09022	561046	S29815	D49851	I61512	A70722	B75318	HB3427	B69009
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28.7	28.7	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.1	28.1	27.8	27.8	27.8
48.5	48.5	48		4 8		48	48	48	48	48	47.5	47.5	47	47	47
0	1	32	33	34	35	98	37	38	39	0	41	2	ñ	44	ເດ

ALIGNMENTS

120011
oc/bo/ projectin-releasing peptide - rat
 C; Species: Rattus norvegicus (Norway rat)
R'Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T
Biochem. Biophys. Res. Commun. 281, 53-56, 2001 A:Title: Isolation and characterization of the rat prolactin-releasing peptide gene: Mul
 A; Reference number: JC7607; MUID:21092785; PMID:11178959
 A. Accession: UC7607
A; Molecule type: DNA
A; Residues: 1-83 < YAM>
 A)cross-reinerices: Dubishaviouz; Dubishaviouz; Dubishaviouz; C:Comment: This bebtide induces arachidonic metabolite release from rat anterior p)
 release, and stimulation of ACTH secretion from the pituitary.
 C;Genetics:
A;Gene: FIRF A;Introns: 33/1
Query Match 99.4%; Score 168; DB 2; Length 83; Best Local Similarity 100.0%; Pred. No. 2.4e-17; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SRAHQHSMETRTPDINPAWYIGRGIRPVGR 30
 Db 22 SRAHQHSMETRTPDINPAWYTGRGIRPVGR 51
RESULT 2 T50904
Mg_protoporphyrin methyl_transferase [imported] - Rubrivivax gelatinosus
 C;Species: Rubritvax getatinosus C:Date: 21-Jul-2000 #secuence revision 21-Jul-2000 #text change 02-Sep-2000
40
R.Nagashima, K.V.; Igarashi, N.; Hardada, O.; Nagashima, S.; Marsuura, K.; Shimada, K. Shinagashima, K.V.; Igarashi, N.; Hardada, O.; Nagashima, S.; Marsuura, K.; Shimada, K.
BUDNITCH to the Babba Data Library, November 1997. Riberrintion: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosyn
 A;Reference number: Z25270
 A) ACCESSION: T55904 A. A. A
A; Wolecule type: DNA
A, Residues: 1-1236 «NAG»
 A, Cross-references: BNB1.24034704; PIDN:BAA94057.1
 Apapethemical source areas that the control of the
 A;Gene: bchH C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
 Query Match Best Local Similarity 37.5%; Pred. No. 1.7;

Matches

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rossiuses: 1-11415 < STO>
A;Cross.veferences: GB:AE004874; GB:AE004091; NID:g9950849; PIDN:AAG07989.1; GSPDB:GN001]
A;Experimental source: strain PAO1
C;Genetics:
A;Gene : PA4601
C;Superfamily: oxygen sensor diguanylate cyclase/c-di-GMP phosphodiesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. strain PCC 7120
C;Date: Nostoc sp. strain PCC 7120
C;Accession: AH2016
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 9, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MuID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE004228; GB:AE003852; NID:g9655997; PIDN:AAF94657.1; GSPDB:GN001.
A;Experimental source: serogroup Ol; strain NI6961; biotype El Tor
C;Genetics:
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Nature 406, 477-483, 2000
A;Title: DNL Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A82193
Sun/nucleolar protein family protein VC1502 [imported] - Vibrio cholerae (strain N16961
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: A81193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Residues: 1-303 «KUR»
A,Cross-references: GB:BA000019; PIDN:BAB78052.1; PID:g17135506; GSPDB:GN00179
A,Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                Score 53; DB 2; Length 1415;
Pred. No. 29;
4; Mismatches 11; Indels
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Pred. No. 6.5;
2; Mismatches
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ilarity 37.5%;
Conservative
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ilarity 48.4%;
Conservative
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Best Local Similarity
Matches 9; Conserv
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nes 15; Conserv
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A,Molecule type: DNA
A,Residues: 1-503 <HEI>
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A;Status: preliminary
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C083070
C083070
C083070
C) Species: Pseudomonas aeruginosa
C; Species: Dseudomonas aeruginosa
C; Species: Dseudomonas aeruginosa
C; Date: 15-Sep-2000
C; Species: Dseudomonas aeruginosa
C; Date: 15-Sep-2000
C; Species: Dseudomonas aeruginosa
C; Date: 15-Sep-2003
C; Accession: C83070
C; Accession: C83070
C; Accession: C83070
C; Accession: C87: Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Braman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin, Nature 406, 959-964, 2000
A; Litle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathola; Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                          probable magnesium chelatase (BC 4.99.1.-) chain H BchH - Heliobacillus mobilis C;Species: Heliobacillus mobilis C;Species: Heliobacillus mobilis C;Species: Heliobacillus mobilis C;Stecies: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000 C;Accession: T31462 R;Xiong, J:; Inoue, K.; Bauer, C.E. R;Xiong, J:; Inoue, K.; Bauer, C.E. Proc. Natl. Acad. Sci. U.S.A. 95, 14851-14856, 1998 A;Title: Tracking molecular evolution of photosynthesis by characterization of a major A;Reference number: Z21036; MUD:99061957; PMD:9843979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AjGene: bohH
C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
C;Keywords: lyase.
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A;Molecule type: DNA
A;Residues: 1-1292 <XIO>
A;Cross-references: EMBL:AF080002; NID:g3820536; PID:g3820560; PIDN:AAC84033.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable unr protein - rat
Cippedes: Rattus norvegicus (Norway rat)
Cippedes: Rattus norvegicus (Norway rat)
Cipate: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
Cipacession: S11210
Rivelfers, M.; Paciucci, R.; Pellicer, A.
Nucleic Acids Res. 18, 4891-4899, 1990
A;Title: Characterization of unr; a gene closely linked to N-ras.
A;Reference number: S11210; MUID:90370473; PMID:2204029
   Gaps
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A;Molecule type: mENA
A;Residues: 1-798 cERE
A;Cross.references: EMBL:X52311; NID:g57454; PIDN:CAA36549.1; PID:g57455
C;Keywords: DNA binding
      9
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   Indels
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Pred. No. 4.9;
                                                     3 AHOHSMETRIPDINPAWYTG-----RGIRPV 28
Mismatches
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12; Conservative
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Best Local Similarity Matches 11, Conserv

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Query Match

Best Local Similarity Matches 10; Conser

d 8

Query Match

5

g ò

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A;Molecule type: DNA
A;Residues: 1-482 <DIE.
A;Gross-references: EMBL:U32274; NID:g927313; PIDN:AAB64830.1; PID:g927321; GSPDB:GN0000f
C;Genetics:
                                                                                                          hypothetical protein F8J2.80 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress)
C;Species: Arabidopsis thaliana (Mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Date: 20-Apr-2000
R;Nyakatura, G; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; Mayer, K.F.X.
Mayer, K.F.X.
Mayer, K.F.X.
A;Reference number: 224458
A;Reference number: 224458
A;Accession: T47748
A;Accession: T47748
A;Accession: preliminary
A;Accession: L-548 cNYA>
A;Residues: 1-548 cNYA>
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AyAccession: S40803

AyRolecule type: DNA

AyRolecule type: DNA

AyCession: S69672

AyCession: S69672
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C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000
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A,Map position: 3
A;Introns: 78/1; 143/1; 242/2; 377/3; 428/2; 447/3; 470/3; 502/3; 532/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 4R
C;Superfamily: RVS167 protein; RVS161 protein homology; SH3 homology
C;Keywords: transmembrane protein
F;4-270/Domain: RVS161 protein homology <RVS>
F;292-422/Region: alanine/glycine/proline-rich
F;428-477/Domain: SH3 homology <SH3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 548;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:AL132969
A,Experimental source: cultivar Columbia; BAC clone F8J2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 1;
Pred. No. 25;
3; Mismatches 5;
SECHQHNVFVYLPAVDDLTKQWFIAHGFEQVG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 SLLHQSPMHFLHPLQHSFPHHQPSWYWGRG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
29.9%; Score 50.5; DE
Best Local Similarity 35.5%; Pred. No. 24;
Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRAHQ-----HSMETRTPDINPAWYTGRG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: SGD:RVS167; MIPS:YDR388w
A,Cross-references: SGD:S0002796; MIPS:YDR388w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 RTPDVN-EWWTGRYNGQQGVFP 473
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Best Local Similarity 50.0%;
Matches 11; Conservative
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        120
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AjAccession: S67150
AjRoleule type: DNA
AjRoleule type: DNA
AjCross-references: EMBL: Z75161; NID: g1420572; PID: e252411; PID: g1420573; GSPDB: GN00015;
AjCross-references: EMBL: Z75161; NID: g1420572; PID: e252411; PID: g1420573; GSPDB: GN00015;
AjCross-references: S70: S0005779
AjCross-references: S70: S0005779
AjMap position: 15R
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A, Cross-references: EMBL: 250873; PIDN: CAA90762.1; GSPDB: GN00028; CESP: F19H6.1
A, Experimental source: clone F17E5
B, Experimental source: clone F17E5
B, McMurray, A.
Submitted to the EMBL Data Library, November 1995
A, Reference number: Z19378
A, Accession: T21124
A, Accession: T21124
A, Experimental sype: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Experimental source: clone F19H6
A, Experimental source: clone F19H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein YOR253w - yeast (Saccharomyces cerevisiae)
Nylternate names: hypothetical protein 05315
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S67150
R;Jauniaux, J.C.; Poirey, R.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67143
                                                                                                                                                                                                                                                     hypothetical protein F19H6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T21075; T21124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: X
A;Introns: 55/3; 85/2; 113/3; 150/1; 192/3; 266/2
C;Superfamily: kinase-related transforming protein; protein kinase homology
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                                     13;
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A, Status: preliminary, translated from GB/EMBL/DDBJ
A, Molecule type: DNA
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                                                                                  1 SRAHQHSMETKIPDINPAWYTGRGIRPVGR 30
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             Pred. No. 16;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, August 1995
A;Reference number: Z19368
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          l Similarity 36.7%;
11; Conservative E
                Local Similarity
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Cyacession: F86019
Iller, L., Grobbeck, E.J., Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A.Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A.Reference number: A85480; MUID:21074935; PMID:11206551
A.Status: preliminary
A.Status: Dreliminary
A.Residues: 1-375 cs70>
A.Cross-references: GB:AE005174; NID:g12518177; PIDN:AAG58618.1; GSPDB:GN00145; UWGP:Z488
C.Genetics: A.Accellation of the control of the co
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A,Molecule type: DNA
A) Expesion of the state of the st
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE000424; GB:U00096; NID:g2367230; PIDN:AAC76510.1; PID:g1789897; A;Experimental source: strain K-12, substrain MG1655 C;Genetics:
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A;Residues: 1-375 <BLAT>
Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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Pred. No. 22;
5; Mismatches
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Pred. No. 22;
5; Mismatches
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Best Local Similarity 47.4%;
Matches 9; Conservative
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Best Local Similarity 47.4
Matches 9; Conservative
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                                                                                                                                                                                            Avcludease ABC chain A - Methanobacterium thermoautotrophicum (strain Delta H)
N.Alternate names: uvrA protein
C.Species: wethanobacterium thermoautotrophicum
C.Species: Methanobacterium thermoautotrophicum
C.Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C.Accession: H69157
R.Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
C.Ju, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wieczbowski, J.; Gibson, R.; Jiwani, N.
J. Bacteriol. 1997 7135-7155, 1997
A.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A.Reference number: A69000; MUID:98037514; PMID:9371463
A.Accession: H69157
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R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. DNA Res. 8, 11-22, 2001
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gency A.Ritle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gency A.Accession: P9173
A.Fature: preliminary
A.Accession: Ppil73
A.Accession: Ppil73
A.Accession: Speciminary
A.Accession: Ppil73
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A.Accession: Ppil73
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A;Experimental source: strain Delta H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-962'<MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 53;
0; Mismatches 4; Indels
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SLETRMRFNPNLDPAWFGG 179
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11 RIPDINPAWYIG

8 엄 RESULT 13 F91173

Query Match

A;Gene: MTH443 A;Start codon: TTG

1;

probable transporter yhhJ [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 C;Species: Escherichia coli

Conservative

Query Match
Best Local Similarity
9; Conserve

161

à ద RESULT 14 F86019

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August 12, 2004, 14:37:35; Search time 8.11047 Seconds (without alignments) 199.024 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                   Run on:
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OM protein - protein search, using sw model

US-09-700-643A-3 169 1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRX 31 Title: Perfect score: 1 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P81278 rattus norv	P81264 bos taurus	P81277 homo sapien	097859 bos taurus											QBnrm3 corynebacte					P26162 rhodobacter	P39429 mus musculu								P73412 synechocyst	Q92iy7 rickettsia	m	Q24629 drosophila	
SOFFICENTES		QI	PRRP_RAT	PRRP_BOVIN	PRRP HUMAN	NER3 BOVIN	UNR RAT	NER3 HUMAN	LMBT_HUMAN	R167_YEAST	UVRA_METTH	YHHJ_ECOLI	Y355_BUCAI	BCHH_RHOSH	CYSC_YERPE	EX71_COREF	EX71_CORGL	NRP1_YEAST	UNR_HUMAN	XPO7_HUMAN	XPO7_MOUSE	BCHH_RHOCA	TRA2_MOUSE	GCSP_MYCTU	TBB2_GEOCN	UVRA_VIBPA	UVRA_VIBVU	T2D3_HUMAN	TRA2 DROVI	TETP_CLOPE	UVRA_SYNY3	QUEA_RICCN	UVRA_VITST	RF2P_DROSI	UVRA_ZYMMO
		B :	-	н	Н	Н	-	Н	н	Н	Н	Н	Н	Н	Н	н	н	Н	н	~	Н	н	Н	Н	-	н	Н	Н	-1	П	Н	Н	Н	H	н
		Length	83	86	87	428	798	428	772	482	962	374	264	1193	213	413	417	719	798	1087	1087	1194	501	941	453	940	940	1083	272	652	970	365	569	599	925
*	Query	Match	99.4	92.8	84.6	.33 1	31.4	30.2	29.9	:29.6	29.6	29.3	29.0	29.0	28.7	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.1	28.1	27.8	27.8	27.8	27.8	27.5	27.5	27.5	27.2	27.2	27.2	27.2
		Score	168	157	143	56	53	51	50.5	20	Ŋ		4,	4		48	48	48	48	48	48	4	47.5	47.5	47	47	47	47	46.5	46.5	46.5	46	46	46	46
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Q8x5u9 escherichia Q8fb02 escherichia P0771 escherichia Q9kws vibrio chol B37434 salmonella Q8x5u streptococc Q99y84 streptococc P44410 haemophilus P57979 pasteurella P72481 streptococc Q978x7 streptococc
UVRA_ECOL5 UVRA_ECOL1 UVRA_VECH UVRA_SALTY UVRA_STRP3 UVRA_STRP3 UVRA_STRP3 UVRA_STRP3 UVRA_FRSMU UVRA_PASMU UVRA_PASMU
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tes 25; Conserv
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                                              98 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                           TPDINPAWYTGRGIRPVGRFGRRRATPRDVTGLGGLSCLPL
DGRTKFSQRG -> SECLTYGKQPLTSFHPFTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hindma S., Habaca Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kutokawa T., Nishimura O., Onda H., Fujino M.;

Nature 393:272-276(1998).

-! FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactorrophs directly to secrete PRL.

-! TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.
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30-MX-2000 (Rel. 39, Last sequence update)
30-MX-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRE) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRE]; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                          AMIDATION (G-53 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                              BY SIMILARITY.
PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
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PROLACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                                  EMBL; AFS21930; AAM82154.1; -...

PIR; UC7607; UC7607.

Alternative splicing.

Signal; Cleavage on pair of basic residues; Alternative splicing.

SIGNAL

PEPTIDE

22 52 PROLACTIN-RELEASING PEPTIDE PRRP31.

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SAMIDATION (G-53 PROVIDE AMIDE GROUI VARSPLIC 33 83 TPDINPAWYIGRGIRPUGRERATIPED TPDINPAMYIGRGIRPUGRERRATIPED GROUI
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Hormone, Amidation, Signal, Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 168; DB 1; Length 83;
Pred. No. 9.7e-18;
institutions as long as its content
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D0C75A264EBE4F29 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199.4%; Score 168; DB ilarity 100.0%; Pred. No. 9.7 Conservative 0; Mismatches
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                                                                                                                    EMBL; AB015418; BAA29026.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          9215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     releasing peptide PrRP20]
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NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            83 AA;
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P81264;
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                                                                                                                                                              Gaps
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Hinnma S., Habbta Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-59426652; PubMed-10498338;
Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,
Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
AMIDATION (G-54 PROVIDE AMIDE GROUP). 08AC35A13B0FA908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sumino Y., Fujino M.;
"Tissue distribution of prolactin-releasing peptide (PrRP) and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION (G-54 PROVIDE AMIDE GROUP). 229A2F3F50CF981B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PPRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                            Score 157; DB 1; Length 98; Pred. No. 4.7e-16; 0; Mismatches 2; Indels
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Pred. No. 4.6e-14;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            87 AA.
                                                                                                                                                                                                                            1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
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                                                                                                                                                                                                                                                                                    23 SRAHOHSMEIRTPDINPAWYAGRGIRPVGR
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                                       10544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
53
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53
9639 MW;
                                                                                                      95.98;
                                                                                                                                93.3%;
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                                                                                            92.9
Best Local Similarity 93.3
Matches 28, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              releasing peptide PrRP20]
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RAHQHSMETRTPDINPAWYTGRGIRPV 28

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                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FSB-2003 (Rel. 41, Last annotation update)
28-Salaidase 3 (EC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
(N-acetyl-alpha-neuraminidase 3).
                                                                                                                                                                                                                                                                                                                      S)
                                                                                                                                                                                                                                                                      "Molecular cloning and characterization of a plasma membrane-associated sialidase specific for gangliosides.";
J. Biol. Chem. 274-5504-5011 (1999).
-!- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl
                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=99143165; PubMed=9988745;
Miyagi T., Wada T., Iwamatsu A., Hata K., Yoshikawa Y., Tokuyama
Sawada M.;
                                                                                                                                                                                                                      SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 1; Length 428;
Pred. No. 1.3;
6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418B34F3245A8F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BNR 1.
BNR 2.
BNR 3.
FRIP MOTIF.
By similarity.
Potential.
Potential.
Potential.
Potential.
Potential.
Potential.
Potential.
Potential.
Potential.
        SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
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                     EMBL; AB008184; BAA75071.1; -.
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Pfam; PF02012; BNR; 3.
Hydrolase; Glycosidase; Membi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.1%;
ilarity 37.0%;
Conservative
                                                                             STANDARD;
                                                                                                                                                            Bos taurus (Bovine).
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388
428 AA;
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                  NCBI_TaxID=9913;
                                                                                             28-FEB-2003 (28-FEB-2003 (28-FEB-2003 (514))
                                                                  BOVIN
NER3 BOVIN
097859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Jeffers M., Pedlicer A.;
Jeffers M., Pedlicer A.;
Characterization of unr; a gene closely linked to N-ras.";
Nucleic Acids Res. 18:4891-4899(1990).
-!- FUNCTION: RNA-binding procein (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 798;
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                                                                                                                                                                                                                                                                                                                                          (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                      798 AA
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                                            EMBL; X52311; CAA36549.1; -.
PIR; S11210; S11210.
HSSP; P15277; IMJC.
InterPro; IPR002059; Cold_shock.
InterPro; IPR008994; Nucleic_acid_OB.
Pfam; PF00313; CSD; 7.
ProDom; PD000621; Cold_shock; 1.
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PROSITE; PS00352; COLD_SHOCK; 4.
RNA-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                                                  STANDARD;
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNR protein.
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NER3 HUMAN
ID NER3 HU
AC Q9UQ49;
DT 28-FEB-
DT 28-FEB-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
28-FEB-2003 (Rel. 41, Last annotation update)
Sialidase 3 (EC 3.2.1.18) (Membrane sialidase) (Ganglioside sialidase)
                                                                                                                    TISSUE=Brain;
MEDLINE=99335353; PubMed=10405317;
Wada T., Yoshikawa Y., Tokuyama S., Kuwabara M., Akita H., Miyagi T.;
"Cloning, expression, and chromosomal mapping of a human ganglioside
                                                                                                                                                                                                                                           Venerando B.,
                                                                                                                                                                                                                                                                                        Biochem. J. 349:343-351(2000).
-!- FUNCTION: Plays a role in modulating the ganglioside content of the lipid bilayer at the level of membrane-bound sialyl glycoconjugates.
-!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Highly expressed in skeletal muscle, testis, adrenal gland and thymus, followed by pancreas, liver, heart and thymus. Weakly expressed in kidney, placenta, brain and lung. MISCELLANEOUS: Optimum pH is 3.8 SIMILARITY: Belongs to family 33 of glycosyl hydrolases. SIMILARITY: Contains 3 BNR repeats.
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                        Monti E., Bassi M.T., Papini N., Riboni M., Manzoni M., Venerand Croci G., Preti A., Ballabio A., Tettamanti G., Borsani G.; "Identification and expression of NEU3, a novel human sialidase associated to the plasma membrane.";
Biochem. J. 349:343-351(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35D1DD9359A78C98 CRC64;
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GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0003824; F:catalytic activity; TAS.
GO; GO:0006689; P:ganglioside catabolism; TAS.
InterPro; IPR020860; GH BNR.
PF02012; BNR; 3.
PHYDIOLASE; Glycosldase; Membrane; Repeat.
                                                                                                                                                                              Blochem. Biophys. Res. Commun. 261:21-27(1999).
                                                                                                                                                                                                                                                                                                                                                                                          SÜBCELLULAR LOCATION: Membrane-associated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
Potential.
By similarity.
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BNR 2.
BNR 3.
FNIP MOTIF.
By similarity.
Potential.
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Potential
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                     (N-acetyl-alpha-neuraminidase 3).
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
PubMed=10861246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140
                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428 AA;
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                     sialidase.
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REGUENCE FROM N.A.

RECURRE-21638749; PubMed=11780052;

REDLINE=21638749; PubMed=11780052;

REDLINE=21638749; PubMed=11780052;

REDLINE=21638749; PubMed=11780052;

REDLINE=21638749; PubMed=11780052;

REDLINE=21638749; PubMed=11780052;

REDLINE=21638749; PubMed=1178052;

REDLINE=21638749; PubMed=117874;

REDLINE=21638749; PubMed=117874;

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REDLINE=21638749; PubMed=1178054;

REDLINE=21638749; PubMed=1178054;

REDLINE=21638749; PubMed=1178054;

REDLINE=21638749; PubMed=117874;

REDLINE=21638749; PubMed=117874;

REDLINE=21638749; PubMed=117874;

REDLINE=21638749; PubMed=1178749;

REDLINE=21638749; PubMed=11787
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ENT. 772 AA. 9941E6; Q9HIG5; Q9UG06; Q9UJB9; Q9Y4C9; Q9Y4E6; Q9HIG5; Q9UG06; Q9UJB9; Q9Y4C9; Q9Y4E8. 2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Lethal(3)malignant brain tumor-like protein (L(3)mbt-like) (L(3)mbt protein Jamar Carl (3)mbt protein (H-1(3)mbt protein) (H-L(3)mbt). L3MBTL, QR L3MBT (RIANG0681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A human homolog of Drosophila lethal(3)malignant brain tumor (1(3)mbt) protein associates with condensed mitotic chromosomes."; Oncogene 18:3799-3809(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koga H., Matsui S.-I., Hirota T., Takebayashi S.-I., Okumura K.,
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDILNE=88403880; PubMed=9734811;
IEDikawa 840.380; Nagase T., Suyama M., Miyajima N., Tanaka A.,
Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koehrer K., Bayer A., Mewes H.-W., Gassenhuber J., Wiemann Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                  DB 1; Length 428;
                                                                                                             Indels
                                                                                                             12;
30.2%; scc. No. s...
33.3%; Pred. No. s...
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 215-772 FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                195 KTRPHSLMIYSDDLGVTWHHGRLIRPM 221
                                                                                                                                                                                              2 RAHQHSMETRIPDINPAWYTGRGIRPV 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISSUE=Brain;
MEDLINE=99373015; PubMed=10445843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 414:865-871(2001).
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                           Query Match
Best Local Similarity
Matches 9: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE=Uterus;
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Wilming L.,
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RA SEQUENCE FROM N.A.

RA JEGG C., Alt-Moerbe J., Andre B., Arnold W., Bahr A., Ballesta J.P.G.

RA Jacq C., Alt-Moerbe J., Andre B., Arnold W., Bahr A., Ballesta J.P.G.

RA Bargues M., Baron L., Becker A., Biteau N., Bloecker H., Blugeon C.,

RA Bargues M., Barant P., Brueckner M., Bultrago M.J., Coster F.,

RA Belaveau T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,

RA Goffeau A., Gomez-Peris A., Granolter C., Hanemann V., Hankeln T.,

RA Hoheisel J.D., Jaeger W., Jimenz A., Johniaux J.L., Kraemer C.,

RA Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,

RA Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,

RA Prydz H., Purnelle B., Rasmussen S.W., Remacha M., Revuelta J.L.,

RA Rieger M., Salom D., Saluz H.P., Salz J.E., Saren A.-M., Schaefer M.,

RA Scharfe M., Schmidt B.R., Schmeider C., Scholler P., Schwarz S.,

Urrestarazu L.A., Verhasselt P., Vissers S., Voet M., Volckaert G.,

RA Waner G., Wamburt R., Wedler E., Wedler H., Woelff S., Harris D.E.,

RA Hamlin N., Hunt S., Jones L., McDonald S., Murphy L., Niblett D.,

RA Araujo R., Aviles B., Berno A., Carpenter J., Chen E., Cherry J.M.,

RA Araujo R., Aviles B., Berno A., Carpenter J., Chen E., Cherry J.M.,

RA Chung E., Duncan M., Hunicke-Smith S., Hyman R.W., Komp C.,

RA Lashkari D., Lew H., Lin D., Nosedale D., Nakahara K., Namath A.,
                                                                                                                                                                                                              isoform 3).

Frida-vsp. 003902.
ARINGHVEWTHVSGKTLWWTVAQLGDLVCSDHLQBGKGILETGV
HSLLCSLPTHLLAKLSFASDSQY -> MIOGBAFLLLTQAD
IVKIMSVKLGPALKIYNAILMFKNADDTLK (in
                                                                                                       ARIVRUTHYSGKTIVWHVAQLGDLVCSDHLQBGKGILBTGV
HSLLCSLPTHLLAKLSFASDSQY -> VRCKRVGDRAGVT
VLKTAGSRCPPQRHFC (in isoform 2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93330299; PubMed=8336735;
Bauer F., Urdaci M., Aigle M., Crouzet M.;
"Alteration of a yeast SH3 protein leads to conditional viability with defects in cytoskeletal and budding patterns.";
Mol. Cell. Biol. 13:5070-5084(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117B03A628826B29 CRC64;
                                                     (in isoform 3)
                                                                                                                                                                                                                                                                                                                                                                                  isoform 4).
/FIId=VSP 003903.
P -> L (IN REF. 1).
LR -> MC (IN REF. 1).
L -> M (IN REF. 1).
S -> P (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEE-1995 (Rel. 31, Created)
01-FEE-1995 (Rel. 31, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Reduced viability upon starvation protein 167.
                                                                                     FTId=VSP 003901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 SECHDFWVNANSPDIHPAGWFEKTGHKLQP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRAHQHSMETRTPDINPA-WY--TGRGIRP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50.5;
Pred. No. 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         772 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                 709
                                                                                                                                                                                                                                                                                 709
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P39743;
              ZN FING
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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ID RIG7 YEAST
DT 01-FEBS
DT 10-OCT-
DE Reducer
GN Sacchas
OC Bucarhas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
              ଚ
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BMBL; AL10279; CAB53714.1; -

BMBL; 289752; CAC16799.1; -

BMBL; 289752; CAC16799.1; -

BMBL; 289752; CAC16799.1; -

BMBL; 289752; CAC16800.1; -

BMBL; AL3031681; CAC17548.1; -

BMBL; AL3031681; CAC17548.1; -

BMBL; AL3031681; CAC17548.1; -

BMBL; AL031681; CAC17548.1; -

BMBL; AL031681; CAC17548.1; -

BMSL; AL031681; CAC17548.1; -

BMSL; AL031681; CAC17548.1; -

BMSL; AL031681; CAC17592; Mbt.

BMS, Q97468; -

BMS, Q97468; -

BMS, Q97468; -

BMS, Q97468; -

BMS, CAC17530; AT C2HC.

BMS, Pfam; PF02820; Mbt; 3.

BMS, MART; SMOD561; MBT; 3.

BMA-binding; Nuclear protein; Repeat; Alternative splicing.

BMA-DOMAIN 349 422 MBT.

TOWAIN 349 422 MBT 3.

TOWAIN 453 526 MBT 3.
                                                                                                                     The human L(3)MBT Polycomb group protein is a transcriptional repressor and interacts physically and functionally with TEL repressor and interacts physically repressive state of genes, probably via a compliant properties and interacts with repressive state of genes, probably via a compliant properties and interacts with repressive 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  telophase.
SIMILARITY: Contains 3 mbt domains.
CAUTION: Ref.3 (CAC18508) sequences differ from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOUS SPECIFICITY: Widely expressed. Expression is reduced in TISSUE SPECIFICITY: Widely expressed. Expression is reduced in colorectal cancer cell line SW480 and promyelocytic leukemia cell line HL-60.

DEVELOPMENTAL STAGE: In interphase cells, it is scattered throughout the nucleoplasm. In mitotic cells, it strongly associates with condensed chromosomes from the prophase to
"Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";
DNA Res. 5:169-176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=09Y468-3; Sequence=VSP_003901, VSP_003902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=29Y468-2; Sequence=VSP_003902;
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UVRA METTH
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Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N., Winant A., Yelton M.A., Botstein D., Davis R.W., Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Hallsworth K., Hawkins J., Hillier L.W., Jier M., Johnson D., Johnston L., Kicaba T., Langston Y., Latreille P., Le T., Mardis E., Kirsten J., Miller N., Mhan M., Pauley A., Peluso D., Rikin L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R., Waeerston R., Albermann K., Hani J., Heumann K., Kleine K., Mewes H.W., Collner A., Zaccaria P., The nucleotide sequence of Saccharomyces cerevisiae chromosome IV.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00018; SH3; 1.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
SWART; SW00721; BAR; 1.
SWART; SW00326; SH3; 1.
SWART; SR00022; SH3; 1.
Cytoskeleton; SH3 domain; Coiled coil; Transmembrane; Actin-binding.
Cytoskeleton; SH3 domain; Coiled coil; Transmembrane; Actin-binding.
DOMAIN 31 64 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIN-BINDING.
MEDLINE=95236199; PubMed=7719850;
Amberg D.C., Basart E., Botstein D.;
"Defining protein interactions with yeast actin in vivo.";
"Nat. Struct. Biol. 2:28-35(1995).
-!- FUNCTION: Component of a cytoskeletal structure that is required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for the formation of endocytic vesicles at the plasma membrane level. Could be implicated in cytoskeletal reorganization in response to environmental stresses and could act in the budding site selection mechanism. Binds to actin.

SIMILARITY: Contains 1 BAR domain.
SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GermOnline; 140880; -.
SGD; S0002796; RVS167
SGD; S0002796; RVS167
GO; GO:0008857; C:actin cortical patch (sensu Saccharomyces); IDA.
GO; GO:000897; P:cytcskeletal protein binding; IPI.
GO; GO:0006897; P:polar budding; IMP.
GO; GO:0007121; P:polar budding; IMP.
GO; GO:0006970; P:response to osmotic stress; IMP.
InterPro; IPR004148; BAR.
InterPro; IPR004148; BAR.
InterPro; IPR004145; SH3.
PFMM; PF03114; BAR.
InterPro; IPR004181; INF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.6%; Score 50; DB 1; Length 482; 50.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 COLLED COIL (POTENTIAL).
427 ALA/GLY/PRO-RICH.
367 POTENTIAL.
513. SH3.
52774 MW, 3F0ABS3EBCC95A5B CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 11;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, M92092; AAA35051.1; -. EBBL; U32274; AAB64830.1; -. PIR; S40887. HSSP, PIS174; Z408.
                                                                                                                                                                                                                                                                                                                                                                                            Nature 387:75-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174
292
344
344
421
482 AA;
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Best Local Similarity
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TRANSMEM
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                     SOLUTION AND DESCRIPTION OF STREET SERVICES OF STRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANS=Delta H;

STRANS=Delta H;

WEDLINE=98037514; PubMed=9371463;

MEDLINE=98037514; PubMed=9371463;

MITTESON D. Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Marison D., Hoang L., Keagle P., Lumm W., Potthier B., Qiu D.,

Marison D., Hoang L., Kagle P., Lumm W., Potthier B., Qiu D.,

Modougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Modougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

T. Complete genome sequence of Methanobaccerium thermoautotrophicum

M. Hartisonal analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

L. PUNCTION: The UVABC repair system catalyzes the recognition and

processing of DNA lesions. UvrA is an AfPase and a DNA-binding

processing of DNA lesions. UvrA is an AfPase and a DNA-binding

processing of DNA lesions. UvrA is an AfPase and a DNA-binding

processing of DNA lesions. UvrA is an AfPase and a CurrA and 2

protein. A damage recognition complex composed of 2 uvrA and 2

protein. A damage recognition complex composed of 2 uvrA and 2

UvrB subunits scans DNA for abnormalities. When the presence of a

lesion has been verified by uvrB, the uvrA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity). Subunity and the search for Subunit; Forms a heterotetramer with uvrB during the search for lesions (By similarity). SubcEllULAR LOCATION: Cytoplasmic (By similarity). SIMCELULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00211; ABC_TRANSPORTER 1; 2.
PROSITE; PS0093; ABC_TRANSPORTER 2; 2.
SOS response; Exciation nuclease; DNA repair; DNA recombination;
DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
Zinc-finger; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                     28-FEB-2003 (Rel. 41, Last annotation update)
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)
UVRA OR MTH443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.6%; Score 50; DB 1; Length 962; llarity 40.5%; Pred. No. 23; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649 656 ALF (1048) 774 C4-TYPE. 962 AA; 108395 MW; 2C0EF7FC41CCD060 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                703 RIPRSNPATYIGVFIHIRELFAQIPEARKRGYRP-GR 738
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ATP (POTENTIAL)
962 AA.
                                                                          Created)
Last sequence update)
Last annotation updat
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HAWAP, MF 00205; -; 1.

InterPro; 1PR00031933; AAA ATPase.

InterPro; IPR001439; ABC transporter.

InterPro; IPR004602; UvrA.

Pfam; PF00005; ABC tran; 2.

ProDom; PD0000006; ABC transporter; 1.

SWART; SM00382; AAA, 2.

TIGRFAMS; TIGR00630; uvra; 1.
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STANDARD;
                                                                      30-MAY-2000 (Rel. 39,
30-MAY-2000 (Rel. 39,
28-FEB-2003 (Rel. 41,
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Les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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ZN FING
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2; Indels

453 ŘÍPDVN-EWWÍCRYNGOOGVFP 473 11 RIPDINPAWYIGR ----GIRP 27

RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential).
-:- SIMILARITY: Belongs to the ABC-2 integral membrane protein family.
-:- SIMILARITY: TO E.COLI YBHR AND YBHS AND TO THE C-TERMINAL OF
E.COLI YHIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIESS. (Laxneri; STRAIN=301 / Serotype 2a;
SPECIESS. (Laxneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272465; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang P., Zhang X., Zhang J., Yang G., Yu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao S., Sandt C.H., Feulner G., Vlazny D.A., Gray J.A., Hill C.W.; "Rhs elements of Escherichia coll K-12: complex composites of shared and unique components that have different evolutionary histories."; J. Bacteriol. 175:2799-2808(1993).
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                                                                                                                                                                                                                                                                                                Bacīeria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=E.COI; STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner I analysis of the Escherichia coll genome. V. DNA sequence of the region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
                                                                   THIJ ECOLI STANDARD; PRT; 374 AA. P31993; PF6703; P76703; P767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U00039; AAB18460.1; ALT_INIT.
EMBL, AE006424; AAC76510.1; ALT_INIT.
EMBL, L02370; AAC61886.1; -.
EMBL, AE016358; AAN44960.1; ALT_INIT.
EMBL, AE016992; AAP19222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=E.coli; STRAIN=K12;
MEDLINE=93259920; PubMed=8387990;
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             Shigella flexneri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDIINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids Buchmara sp. APS."
Mature 407:81-86(2000).
--- SIMILARITY: BELONGS TO THE TAID DNASE FAMILY. STRONG, TO E.COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   symbiotic bacterium).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
InterPro; IPR000412; ABC transpt2.
PROSITE; PS00890; ABC2 MEMBRANE; 1.
Hypothetical protein; Transport; Transmembrane; Inner membrane;
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InterPro; IPR001130; TatD_DNase.
Pfam, PF01026; TatD_DNase. 1.
FIGREAMS; TIGR0010; 1.
FROSITE; PS01137; TATD_1; 1.
PROSITE; PS01090; TATD_2; 1.
PROSITE; PS01091; TATD_2; 1.
PROSITE; PS01091; TATD_3; FALSE NEG.
PROSITE; PS01091; TATD_3; FALSE NEG.
SEQUENCE 264 AA; 30520 MW; 7F1DA900018E0AAC CRC64;
                                                                                                                                                                                                                                                                           DB 1; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 264;
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                                                                                                                                                                                                          POTENTIAL.
02895FB13F493391 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
0-OCT-2001 (Rel. 40, Last annotation update)
Putative deoxyribonuclease BU355 (EC 3.1.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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45.0%; Pred. No. 8.2;
ive 6; Mismatches
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                                                                                                                                                                                                                                                                             Score 49.5;
                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                41061 MW;
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NCBI_TaxID=118099;
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                                                                                                                                                                                                                                                                                                                              9; Conservative
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                                                                                                                                                                                                            343
374 AA;
                                                                                                                                                                                                                                                                                                 Similarity
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                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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P57436;
                                                                                           TRANSMEM
TRANSMEM
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                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                             Query Match
Best Local
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Y355_BUCAI
                                                                                                                                                                                                                                                                                                                           Matches
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Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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PHOSPHOSERINE INTERMEDIATE
(BY SIMILARITY).
3CBF16816AAC383F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the APS kinase family.
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Pred. No. 7.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ414156; CAC92594.1; -. EMBL; AE013685; AAM84410.1; ALT_INIT.
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NP BIND 47 54 ATP (1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Exonuclease VII large subunit) XSEA OR CE1078.
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10-0CT-2003 (Rel. 42, Last seq
10-0CT-2003 (Rel. 42, Last ann
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ilarity 47.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            branch; second step.
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es 10; Conserv
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Q8FQP1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                sphaeroides 2.4.1.";
Nucleic Acids Res. 28:862-867(2000).
-!- FUNCTION: INVOLVED IN CHLOROPLAST PIGMENT BIOSYNTHESIS; INTRODUCES
A MAGNESIUM ION INTO PROTOPORPHYRIN IX TO YIELD MG-
                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Magnesium-chelatase subunit H (Mg-protoporphyrin IX chelatase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDILNES-2015.991; PubMed=10648776;
Choudhary M., Kaplan S.,
"DNA sequence analysis of the photosynthesis region of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CO-92 / Blovar Orientalis;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTOROPORPHYRIN IX.
PATHWAY: Light-independent bacteriochlorophyll biosynthesis.
SIMILARITY: Belongs to the Mg-chelatase subunit H family.
                                                                                                                                                                                                                                         Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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Adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF195122; AAF24273.1; -.
PIR; T50729; T50729.
InterPro; IPR003672; Cobn/Mg_chltase.
Pfam; PF02514; Cobn-Mg_chel; 1.
Photosynthesis; Bacteriochlorophyll biosynthesis.
SEQUENCE 1193 AA; 129205 MW; 13DDBBD375223151 CRC64;
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                                                             1193 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
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Pred. No. 4
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                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
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28-FEB-2003 (Rel. 41, Last seq
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CYSC OR YP03364 OR Y0825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.0
Best Local Similarity 33.3
Matches 10, Conservative
                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia pestis
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                                                             BCHH RHOSH
Q9RFDS;
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CYSC YERPE
AC Q8ZBF3;
DT 28-FEB-
DT 10-OCT-
DE Adenyl,
DE Adenyl,
DE S, Chosp
DE S, Chosp
DE CYSC OF
DE AGENYL,
DE CYSC OF
C
                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Pethreston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.Ç., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
Perry R.D.;
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davies P., Dougan G., Leather S., Moule S., Oyston P.C.F., Quail K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Mhitehead S., Barrell B.G., Mature 413:523-527(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-!- FUNCTION: Catalyzes the synthesis of activated sulfate.
-!- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'-
phosphoadenylylsulfate.
-!- PATHWAY: Sulfate activation; cysteine biosynthesis reductive
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10-OCT-2003 (Rel. 42, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
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InterPro; IPR002891; APS kinase.
Pfam; PF01583; APS kinase; 1.
Profon, P0002350; APS kinase; 1.
TIGR0455; apsk; 1.
Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
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us-09-700-643a-3.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.", Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity).
-!- CARALVITIC ACTIVITY: Exonucleolytic cleavage in either 5- to 3'- or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
-!- SUBMIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                             -i- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity).
-!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'- or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
-!- SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                        "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";
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B
                                            Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.4%; Score 48; DB 1; Length 413; 52.4%; Pred. No. 18;
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InterPro; IRR003753; Exonuc VII L.

InterPro; IRR00894; Nucleic acid OB.

Pfam; PF02601; Exonuc VII L; 1.

ITGRFAMS; TIGR00237; xseA; 1.

Hydrolase; Nuclease; Exonuclease; Complete proteome.

SEQUENCE 413 AA; 45171 MW; D3BABD9687C6EEED CRC64;
                                                                                                                                                                                                                                                                                       similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the xseA family.
SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 AA.
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP005217; BAC17888.1; ALT_INIT
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                                                                                                                                                              Genome Res, 13:1572-1579(2003)
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Best Local Similarity
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EX7L_CORGL
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CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: Belongs to the xseA family.

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CC entities requires a license@isb-sib.ch).

CC entities requires a license@isb-sib.ch).

DR HAMAP, MF 00378; -; 1.

DR HAMAP, MF 003
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Q9X3H6
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                   Preproprolactin-releasing peptide.
Ovis aries (Sheep).
Bukaryota; Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF450453; AAL47178.1; -.
SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAAB5 CRC64;
                                                                                                              01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
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Matches 28; Conservative
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PRT; 117 AA PRELIMINARY; Q9W624 Q9W624; RESULT 2 Q9W624 22555

Last sequence update)
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mechanisms and effects (Proceedings of the 11th international congress on photosynthesis), pp.4:2889-2892, Kluwer Academic Publishers,
                                                           MEDLINE-22670508;
MEDLINE-22670508;
KOVACS A.T., Rakhely G., KOVACS K.L.;
KGenes Involved in the Biosynthesis of Photosynthetic Pigments in the "Genes Involved in the Biosynthetic Bacterium Thiocapsa roseopersicina.";
Purple Sulfur Photosynthetic Bacterium Thiocapsa roseopersicina.";
Appl. Environ. Microbiol. 633093-3102 (2003).
EMBL; AF528191; AAP59023.1; -.
SEQUENCE 1245 AA; 136300 MW; 6D2A0D451AD1E437 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K.,
Parot P., Vermeglio A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=IL144;
Nagashima K.V., Shimada K., Matsuura K.;
Phylogenetic analysis of photosynthetic genes of Rhodocyclus gelatinosus: Possibility of horizontal gene transfer in purple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Comamonadaceae; Rubrivivax.
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Igarashi N., Shimada K., Matsuura K., Nagashima K.V.;
"Photosynthetic gene cluster in purple bacterium, Rubrivivax
                                                                                                                                                                                                               Length 1245;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                               37.9%; Score 64; DB 2;
40.6%; Pred. No. 1.5;
iive 5; Mismatches
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MEDLINE=94132007; PubMed=8300574;
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Matches 13; Conservative
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(In) Garab G. (eds.);
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NCBI_TaxID=1058;
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           Carassius auratus (Goldfish).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCEI_TaxID=7957;
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Rhodospirillaceae; Rhodospirillum.
NCBI_TaxID=1085;
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Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales,
Chromatiaceae, Thiocapsa.
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Satake H., Minakata H., Fujimoto M.;
Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF anide) ";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1;
SEOUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
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                                                                                                                                                                                                                                                                     59.8%; Score 101; DB 13;
56.0%; Pred. No. 2.8e-07;
iive 8; Mismatches 3;
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43.8%; Pred. No. 0.19;
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Best Local Similarity 43.8
Matches 14; Conservative
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les 14; Conservative
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RESULT 3

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Q7X3H6;

RESULT 4 07X3H6 1D 07X3 AC 07X3 DT 01-0 DT 01-0 DE BCHH GN Thio OS Thio

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Q7VSA1;
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MEDLINE=99061957; PubMed=9843979;
MEDLINE=99061957; PubMed=9843979;
Xiong J., Inoue K., Barar C.E.;
Xiong J., Inoue K., Barar C.E.;
Tracking molecular evolution of photosynthesis by characterization of a major photosynthesis gene cluster from Heliobacillus mobilis.";
Proc. Natl. Acad. Sci. U.S.A. 95:14851-14856(1998).
EMBL, AF080002; AAC84033.1; -.
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MEDLINE=21822612; PubMed=11832943;
Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
"Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
Nature 415:630-633(2002).
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Heliobacillus.
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                                                                                                                                                                         36.1%; Score 61; DB 2; Length 1236; 37.5%; Pred. No. 4.2;
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GO; GO:0009058; P:biosynthesis; IEA.
InterPro; IPRO0572; CobN/Mg_chltase.
Pfam; PF02514; cobN-Mg chel; 1.
SEQUENCE 1253 AA; 137586 MW; C99ABC010E261511 CRC64;
                                                                                                                                 1236 AA; 134729 MW; 84051C045638520C CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CObN/magnesium chelatase family protein.
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uncultured proteobacterium.
Bacteria; Proteobacteria; environmental samples.
NCBI_TaxID=153809;
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           GO; GO:0016740; F:transferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0009058; P:biosynthesis; IEA. InterPro; IPR003672; CobN/Mg_chltase. Pfam; PP02514; cobN-Mg_chel; 1. Transferase. SEQUENCE 1236 AA; 134729 MW; 84051C04563
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Best Local Similarity 37.5
Matches 12; Conservative
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Matches
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Q8RTV7
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STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
STRAIN=22827954; PubMed=12910271;
MEDLINE=22827954; PubMed=12910271;
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
VCBI_TaxID=51511;
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Alcaligenaceae; Bordetella.
                                                                                                                             Length 1292,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Imai K.S., Satch N., Satcu Y.;
"Ciona savignyi genes.";
"Ciona savignyi genes.";
submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ABOSTYTY, BAB68356.1, -.
InterPro; IPR007087; Znf C2H2.
Pfam; PF00006; Zf C2H2; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2.1; 3.
PROSITE; PS01057; ZINC_FINGER_C2H2.2; 4.
Metal-binding; Zinc, Zinc-finger.
SEQUENCE 355 Ap; 40876 MW; ES8FSDEDDB12EBAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
GO; GO:0009058; P:blosynthesis; IEA.
InterPro; IPR003672; CobN/Mg_chltase.
Pfam; PF02514; cobN-Mg_chel; 1.
SEQUENCE 1292 AA; 144854 MW; 323AA0517B07448D CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                   DB 2;
12;
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                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                             1176 ETRIKILNPKWYEGMLKHGYEGVREI 1201
                                                                                                                                   Score 58;
Pred. No.
                                                                                                                                                                                                                                          9 ETRIPDINPAWYIG-----RGIRPV 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q95Y9;
01-DEC-2001 (TrEMBLrel. 19, C)
01-DEC-2001 (TrEMBLrel. 19, Ls
01-MR-2003 (TrEMBLrel. 23, Ls
zic related protein la.
CS-ZICRIA.
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                                                                                                                                      Query Match
Best Local Similarity 42.3%;
Matches 11; Conservative
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MGD; MGI:1917888; 5730507A09Rik.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 TPDINPAWYTGRGIRP 27
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                                                                                                                                     Query Match
Best Local Similarity 50.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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nes 8; Conservative
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Homo sapiens (Human).
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060687
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Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.; Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica."; Mat. Genet. 35.32-40 (2003). Hydrolase; Complete proteome.

SEQUENCE 314 AA; 33764 MW; A90870683CSBEOB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CS-PH/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
The FANYOM COnsortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
MANALYSIS of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK017751; BAC25529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                   32.0%; Score 54; DB 16; Length 314; 54.5%; Pred. No. 9.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0J479J7.3 (Sushi-repeat protein (SRPUL)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Weakly similar to hypothetical protein KIAA0574.
5730507A0SRIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 SMAGRTPAIEPGWVRQIGIRSV 185
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 54.5%;
Matches 12; Conservative
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Best Local Similarity
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SEQUENCE
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2726Y1
1D CASEY1
AC 0726Y
DT 01-0C
DT 
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Q8BHP9
ID Q8BHP
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Huang C.-H., Chen H., Peng J., Chen Y.;

"Cloning and characterization of the sushi-repeat containing protein (SRP) as a novel interaction partner of Rh type C glycoprotein (RRCS).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kurosawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
Rakestraw K.M., Naeve C.W., Look T.A.,
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                      Score 53; DB 11; Length 139;
Pred. No. 5.6;
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                                                                                                                                                 Indels
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EMBL, AF080618, Pelectron transport, IEA.
GO, GO1006118, Pelectron transport, IEA.
InterPro; IRR001128, Cytochrome_P450.
InterPro; IRR001436, Sushi_SCR_CCP.
Pfam; PF02494; HYR; 1.
Pfam; PF00044; Sushi_3, PR08187F13EFB8 CRC64;
SEQUENCE 465 AA; 52971 MW; 4D752B187F73EFB8 CRC64;
Hypothetical protein.
SEQUENCE 139 AA; 14740 MW; A08DD1B09441B259 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Sushi.repeat protein (Sushi.repeat containing protein)
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                   31.4%; scc. No. 50.0%; Pred. No. 5...
                                                                                                                                                                                                                                                                                                                                                                                                              465 AA
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"Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDAIIO.";

DNA Res. 9.189-197(2002).

EMBL; APONGS939; BAC4409.1; -.

R GO; GO:0005524; F:DNA ligase (ATP) activity; IEA.

GO; GO:000521; F:DNA ligase (ATP) activity; IEA.

GO; GO:0006281; P:DNA recombination; IEA.

R GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006280; P:DNA replication; IEA.

R ThterPro; IRRO0997; DNA_ligase.

R PROSITE; PS00697; DNA_ligase.

R PROSITE; PS00697; DNA_LIGASE_AI; I.

COMPLETE PROSOFOR DNA_LIGASE_AI; I.

COMPLETE PROSOFOR DNA_LIGASE_AI; I.

R PROSITE; PS00697; DNA_LIGASE_AI; I.

COMPLETE PROSOFOR DNA_LIGASE_AI; I.

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COMPLETE PROSOFOR DNA_LIGASE_AI; I.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22484998; PubMed=12597275;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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Best Local Similarity 38.7%; Pred. No. 31;
Matches 12; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
Ouery Match 31.4%; Score 53; DB 4; Length 465; Best Local Similarity 50.0%; Pred. No. 22; Matches 8; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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089VA3
AC 089VA3
AC 089VA
AC 089VA
DT 01-JU
DT 
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240 HEVELIMPGLAPPYLDLFAMLEGRGEKPVNR 270

6 HSMETRIPDINP-----AWYTGRGIRPVGR 30

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689 AA

PRT;

PRELIMINARY;

QBR3R1 QBR3R1;

RESULT 15 QBR3R1 ID QBR3R: AC QBR3R:

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L Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

L Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

- I-STMILARITY: BELOAD.

R GO, GO:0003677; F:DNA binding; IEA.

R GO, GO:0004601; F:peroxidase activity; IEA.

R GO, GO:0006979; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR002019; Poroxidase.

R InterPro; IPR002016; Peroxidase.

R InterPro; IPR002016; Peroxidase.

R PROSITE; SO00451; CSD; 4.

B RROSITE; PS00456; PEROXIDASE_2; 1.
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                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VCBI_TaxID=10090;
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Best Local Similarity 43.5%; Pred. No. 34;
Matches 10; Conservative 5; Mismatches 8; Indels
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Mus musculus (Mouse)
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AAG62523 AAB73370 AAW513870 AAW51881 AAW87613 AAW5218 AAX4929 AAX4929 AAX4929 AAX4929 AAX10347 AAX1372 AAW31372 AAW31372 AAW31372 AAW3189

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August 12, 2004, 14:37:35 ; Search time 65.7849 Seconds (without alignments) 133.146 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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169
1 SRAHQHSMETRTPDINPAWYIGRGIRPVGRX
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Maximum Match 100%
Listing first 45 summaries
                                                                 protein search, using sw model
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1. geneseqp1980s:*
2. geneseqp200s:*
4. geneseqp2001s:*
5. geneseqp2001s:*
7. geneseqp2003as:*
7. geneseqp2003bs:*
8. geneseqp2003bs:*
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Gapop 10.0 , Gapext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Rat type
Murine pi
Rat 1992
Rat 1992
Rat type
Rat brola
Rat oxyto
Peptide p
Rat CRH r
Rat ERPPeptide p
Rat CRH r
Rat CRH r Description Adw31384 | Adw89174 | Adw895174 | Adw895174 | Adw895174 | Adw895173 | Adw895172 | Adw895172 | Adw995172 | Adw995183 | Adw995172 | Adw995183 | Adw99525 | Adw995183 | Adw99525 | Adw995183 | Adw99525 | Adw995183 | Adw99525 | Adw9 AAW31384
AAW95174
AAW95174
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AAW87614
AAB10355
AAR87809
AAG62524
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AAW31386 ЭВ **UMMW44566UM460M4** Query Match Length Score Result No.

RESULT 45 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	42 159 44 159 45 159 45 159 45 159 150 150 150 150 150 150 150 150 150 150		N 00 00 01	0000 0000 0000 0000 0000 0000 0000 0000 0000	 Ti	23.2 3.3 2.3 2.4 4.5 4.5 4.5 4.5 4.5 4.5 4.5 4.5 4.5 4		ABUG0832 AAW31373 AAW95190 ALIGNN ALIGNN	6031 31373 95190 ALIGNMENTS AA.		Abu 60832 Aaw 95190 Aaw 95190	3 Bov	Peptide p Bovine G Bovine pi	
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X S	Rattus	es sp.												
XX PN	W0972	WO9724436-A2	8											
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PF	26-DE	6-DEC-1996		0.	96WO-JP003821	P00	382	J.						
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XX Id Id	Hinuma Kitada	ຜູ້ ດີ,	Ha	Habata	ta Y,	Ka	Kawamat	ata Y,	Hosoya M,	Fujii R,	, Fukusumi		., S	
X	WPI; N-PSD	WPI; 1997-363672/33 N-PSDB; AAV02421.	63	67.	2/33. 1.									
XX	Ligand function	Ligand peptide f function in the	t d	h e	for G	pro	tei ner	protein-coupled	or G protein-coupled receptor - 6 central nervous system, pancreas	and	by modulating pituitary gland	ating y gla	and.	
X X	Clain	Claim 2; Pa	ge	+	Page 179; 25	8pp	Ξ.	258pp; English.						
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                consciousness, anxiety syndroune, achicophrenia, trauma, growth horemose consciousness, anxiety syndroune, schizophrenia, trauma, growth horemose secretory disease, hyper- and polyphagia, hyperprolactinaemia, diabetes, hypercholesterolaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthitis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute mycocardial infraction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein. (Updated on 27-AUG-2003 to correct OS field.)
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  depression, hyperkinetic syndrome, disturbance
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0
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Pred. No. 1.5e-17;
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100.0%; Pred. No. 1.-
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Matches 30; Conserv
                                                                                                                                                                                                                                                                                              Sequence 31 AA;
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AAW95174
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Murine pituitary-derived ligand polypeptide antigenic epitope. AAW95174 standard; protein; 31 AA (first entry) 10-MAR-1999

Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer; disease; Parkinson's disease; Huntington's disease; drug; Creuzzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; epitope.

Mus sp.

WO9849295-A1.

05-NOV-1998,

98WO-JP001923 27-APR-1998;

97JP-00109974 28-APR-1997;

(TAKE) TAKEDA CHEM IND LID.

ŝ Fukusumi Hinuma S,

WPI; 1999-009423/01

New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or URR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, Disclosure; Page 26; 206pp; English. drug screening.

This represents the matured murine pituitary-derived ligand polypeptide sequence. The polypeptide is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the

Disclosure; Page 134; 206pp; English.

drug screening

ö e.g. to treat semile dementia, Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia, disorders of growth hormone secretion; cancer; rheumatoid arthritis, epilepsy and many others, also to improve postoperative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antiseas, in drug development; for gene therapy and to develop transgenic animals. Sequences AAW95174 to AAW95178 represent antigenic epictpes which can be used for the preparation of anti-ligand polypeptide antibody Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; soreen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and Gaps ó, Murine pituitary-derived ligand mature polypeptide sequence. Length 31; Indels 99.4%; Score 168; DB 2; L 100.0%; Pred. No. 1.5e-17; Live 0; Mismatches 0; 1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30 1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30 gene therapy; transgenic animal. AAW95173 standard, peptide, 31 97JP-00109974. (TAKE) TAKEDA CHEM IND LTD (first entry) Conservative ŝ WPI; 1999-009423/01. Similarity Sequence 31 AA; Local Sim-27-APR-1998; 28-APR-1997; 10-MAR-1999 WO9849295-A1 05-NOV-1998. Hinuma S, AAW95173; Query Match Matches RESULT 3 886666666666666888 ઠે ద

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amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis, epilepsy and many hormone secretion; cancer; rheumatoid arthritis, epilepsy and many vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide encoding expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy
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                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing a 19P2 pituitary G protein receptor ligand - by cleavage of fusion protein, useful for preventing and treating dementia, breast cancer, renal failure and autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19P2 ligand; G protein coupled receptor; pituitary; prolactin releasing peptide; rat; dementia; breast cancer; therapy.
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                                                                                                                                                                                                                                                  99.4%; Score 16%; DB 2; Length 31; 100.0%; Pred. No. 1.5e-17; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                 1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAW87614 standard; peptide; 31 AA.
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                                                                                                                                                                                          to develop transgenic animals
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                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                        Sequence 31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat 19P2 ligand
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This is the amino acid sequence of the rat pituitary G protein-coupled receptor ligand 1992L. A method suitable for commercial high-level production of 1992L comprises expressing the ligand in host cells as a recombinant fusion protein e.g. with human basic fibroblast growth factor (see AAV87794-95) that has been modified to include an N-terminal cysteine residue. The ligand is released from the fusion by cyanylation followed by ammonolysis. 1992L has prolactin secretion-stimulating and clar high doses) prolactin secretion-inhibiting properties. It can be used dementia, crebrovascular dementia, and dementia associated with: mile per applicat disorders (e.g. Alzheimer's disease, Parkinson's disease, Pick's disease, Huntington's disease, printington's disease, Creutzfeldt-Jakob's), endocrine or metabolic disease or toxicosis (e.g.

Claim 5; Page 34; 56pp; English.

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hypothyroidism, vitamin B12 deficiency, alcoholism, intoxication by drugs, metal and organic compounds) tumourigenic diseases (e.g. brain cutmour), traumatic diseases (e.g. chronic subarachonidal heamorrhage, and other types of dementia, depression, hyperactive child syndrome (microencephalopathy) and disturbance of consciousness. It is also useful for prevention and treatment of diseases associated with prolactin hypo and hypersecretion respectively, including: hyperprolactinaemia, pituitary adenoma, breast cancer, infertility, impotence and autoimmune disease (hypersecretion disorders), and seminal vesicle hypoplasia, osteoporosis, menopausal syndrome and renal failure (hyposecretion disorders) and seminal as a test reagent for study of the prolactin secretory function or as a lactogogue in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat type ligand, modulation, prolactin secretion; genecyst cacogenesis; menopausal syndrome; euchyroid; hypometabolism; lactation; pitultary adenomatosis, brain tumour; emmeniopathy; autoimmune disease; prolactinoms; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Porbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy.
                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                            99.4%; Score 168; DB 2; Length 31; 100.0%; Pred. No. 1.5e-17; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat type ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW97233 standard; peptide; 31 AA.
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Best Local Similarity 100.
Matches 30; Conservative
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                                                                                                                                                                                                                                                     mammalian farm animals
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                                                                                                                                                                                                                                                                                            Sequence 31 AA;
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hypocovarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, imporence, amenorthea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo Syndrome, Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyscoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choricoarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAV49290-302 represent peptide fragments of the 19P2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in diagnosis, as drugs and in studying
                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                               Length 31;
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                                                                                                                                                                                                                                                                           99.4%; Score 168; DB 2; Lilarity 100.0%; Pred. No. 1.5e-17; Conservative 0; Mismatches 0;
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diseasês related to ligand abnormality
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                           Sequence 31 AA;
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Modified-site
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Sequence 31 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying modulators of body weight by a combination of a cell-free or cell-based assay to identify modulators of GPR10, followed by an in vivo assay for the compounds effect on e.g. feeding behavior.
                                                                                                                                                                                                                                                                                                            Prolactin-releasing peptide; PrRP; GPR10; G protein-coupled receptor; feeding behaviour; food intake; modulation; antagonist; anorectic; obesity; agonist; cachexia.
                                 Gaps
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99.4%; Score 168; DB 3; Length 31;
100.0%; Pred. No. 1.5e-17;
                               Indels
          100.0%; Pred. no.
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                                                                                                                                                                                                                                                                                Rat prolactin-releasing peptide, PrRP.
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                                                                                                                                                                                AAY87504 standard; protein; 31
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98US-00172353.
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                 Similarity
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Modified-site
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Query Match
                 Best Local
Matches 3
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hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                  10-SEP-1999;
15-OCT-1999;
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                                  Synthetic
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                                                                                                                                               COW;
                                                                                                                                                                                                                                                                                                                                                                     Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
                                                                                                                               Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; or caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
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                                                                                                           Rat oxytocin secretion promoting peptide SEQ ID NO: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
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                                         AAB10355 standard; peptide; 31 AA
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                                                                                                                                                                                                                                                                                                    (TAKE ) TAKEDA CHEM IND LTD.
                                                                                    24-NOV-2000 (first entry)
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Les 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-452298/39.
                                                                                                                                                                                                             WO200038704-A1.
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                                                                AAB10355;
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The present invention describes a modified therapeutic peptide (I)

comprising a therapeutically active amino acid region (III) and a

reactive group (II) (e.g. succinimidyl and maleimido groups) attached to

a less therapeutically active amino acid region (IV), which covalently

bonds with amino/Nydroxyl/thiol groups on blood components to form a

comprision of the reactive operation of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth

control freatment of various disorders. Endogenous therapeutic

cytvo for the treatment of various disorders. Endogenous therapeutic

cytvo for the treatment of various disorders. Endogenous therapeutic

cytvo for the treatment of active and and adders as they require frequent

control from a traching therapeutic peptides of allowing prevents or

condition and attaching therapeutic peptides to albumin prevents or

creduces the action of peptideses to increase length of activity (half

condition and specificity as bonding to large molecules decreases

condition of AAB92441 represent peptides which can be used in the

exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
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                                                                                                                                                                                                                                                                                                                 Holmes DL,
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                                                                                                                                                                                                                                                                                                                      Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG62524 standard; peptide; 31 AA
                                                                   99US-0134406P.
99US-0153406P.
99US-0159783P.
17-MAY-2000; 2000WO-US013576
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                                                                                                                                                                                                                                     (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                      Ezrin AM,
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Best Local Similarity
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Kitada C,

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The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolatcin releasing peptide (PrRP) receptor (CPR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizuress and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. PrRP receptor agonists may be used to treat common disorders which lead psychogenic hypersomnia. PrRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep and siscered and psychophysiologic insomnia. The present sequence is rat prRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a
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for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide production by gene recombination associated peptide #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide production, low-molecular peptide, KiSS-1, GPR8 ligand, gene recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.4%; Score 168; DB 5; Length 31; 100.0%; Pred. No. 1.5e-17; ive 0; Mismatches 0; Indels
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                                                                                                   Disclosure; Page 24; 35pp; English.
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Best Local Similarity 100.
Matches 30, Conservative
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                                                                                                                                                                                                                                                                                                                   Use of G protein receptor ligand or peptide for controlling corticotropin
                                                                                                                                                                                                                                                                                                                                                                                                                                                        corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; wakefulness; sleep disorder; prolactin releasing peptide receptor; PrRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea; insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure; anticonvulsant.
                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence describes a method of controlling the secretion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for compounds useful for promoting wakefulness or sleep, and
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                                                                                                                                                                                                                         Matsumoto H, Hinuma S;
                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 69; 90pp; Japanese.
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                                                           17-NOV-2000; 2000WO-JP008119
                                                                                                        99JP-00327900
2000JP-00297073
                                                                                                                                                                                                                                                                                                                                              releasing hormone secretion.
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1es 30; Conservative
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                                                                                                        18-NOV-1999;
26-SEP-2000;
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Rattus sp

AAE26400;

RESULT 11 AAE26400 ID AAE2

Query Match

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protein-coupled receptor; ligand binding; pharmaceutical; modulator; tuitary; central nervous system; pancreas; prophylactic;
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                                                                                                                  Rat type G protein-coupled receptor ligand fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                               Habata Y, Kawamata Y, Hosoya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 179; 258pp; English.
                         standard; peptide; 32
                                                                                                                                                                                                                                                                                                   95JP-00343371.
96JP-00059419.
96JP-00211805.
96JP-00246573.
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                                                                                                                                                         pituitary; .....therapeutic agent.
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18-SEP-1996;
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15-MAR-1996;
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06-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a trarget peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides of St. 1 peptide and GPRS ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
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precursor protein with specific cleavage sites. With this method, pe production can be carried out easily to provide large quantities of required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
                                                                                                                                                                                                                                                                                                                  Peptide production by gene recombination associated peptide #21
                                                                                                                                                                                                                                                                                                                                          Peptide production; low-molecular peptide; KiSS-1; GPR8 ligand;
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                                                                                         Length 31;
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Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 30; Conservative 0; Mismatches 0;
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.larity 100.0%; Pred. No. 1.5e-17;
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                                                                                                                                                                                                                                    ABU60837 standard; peptide; 31
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Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                        gene recombination
                                                                 AA;
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                                                                                                                                                                                                                                                                                         06-MAY-2003
                                                                Sequence 31
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This sequence represents a peptide fragment from a novel rat type ligand polypeptide corresponding to amino acid residues 22 to 53 of the sequence represented in AAW11383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituiery function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone serestory disease, hyper and polyphagia, hyperlipidaemia, diabetes, hypercholesterolaemia, hyperchylveridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, concerpendia clateral schemaia, hyperprolactinaemia, epilepsy, amylotrophic lateral schemaia, proceedia in julyy, transient brain ischaemia, epilepsy, amylotrophic lateral schemaia, bone fracture, trauma, atopic dermatitis, consciousnes and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the lighdated on 27-AUG-2003 to correct OS field.)
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RESULT

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This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of futuse for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion
                                                                                                                                                              Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
99.4%; Score 168; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                Rat oxytocin secretion promoting peptide SEQ ID NO: 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 57; 72pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsumoto H, Kitada C, Hinuma S;
                 AAB10356 standard; peptide; 32 AA
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                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                   WO200038704-A1
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                                                                                         24-NOV-2000
                                                                                                                                                                                                                                                                                                                                    06-JUL-2000.
                                                                                                                                                                                                                                                               Rattus sp.
                                                       AAB10356;
AAB10356
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Gaps . 0

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Search completed: August 12, 2004, 14:43:55 Job time : 66.9099 secs

Sequence 92, Appl Sequence 78, Appl Sequence 7, Appl Sequence 17, Appl Sequence 27, Appl Sequence 16, Appl Sequence 16, Appl Sequence 18, Appl Sequence 2047, Appl Sequence 2047, Appl Sequence 2047, Appl Sequence 160071, Sequence 160069, Sequence 153474, Sequence 153474, Sequence 160069, Sequence 160069, Sequence 153474, Sequence 150069, Sequence 53922, Appl

Sequence 88, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 78, Appl Sequence 17, Appl Sequence 16, Appl Sequence 16, Appl

Sequence

Run on:

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Query Match 99.4%; Score 168; DB 9; Length 31; Best Local Similarity 100.0%; Pred. No. 1e-16; Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09932161
Patent No. US20020037533A1
Patent No. US20020037533A1
GENERAL INFORMATION:
APPLICANT: Lin, Steven
APPLICANT: Lin, Steven
TITLE OF INVENTION: Premeing and Therapeutic Methods For TITLE OF INVENTION: Premeing Makefulness and Sleep
FILE REFERENCE: P-UC 4679
CURRENT FELLIG DATE: 2001-08-17
PRIOR PILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
13 US-10-044-592-82
13 US-10-044-592-84
13 US-10-044-592-86
13 US-10-044-592-86
13 US-10-044-592-86
14 US-10-044-592-86
15 US-10-044-592-86
16 US-10-095-777-15
17 US-10-095-777-17
18 US-10-044-592-6
19 US-10-096-777-17
19 US-10-094-592-6
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US-10-301-822-197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Rattus
US-09-932-161-14
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US-10-044-592-4
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LENGTH: 31
TYPE: PRT
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                                                                                                                                                                                     August 12, 2004, 14:49:10 ; Search time 54.7907 Seconds (without alignments) 177.617 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_RW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_RW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBGOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBGOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-044-592-4
US-10-0064-752-15
US-10-0064-592-10
US-10-044-592-10
US-10-044-592-96
US-10-044-592-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                   1 SRAHQHSMETRTPDINPAWYTGRGIRPVGRX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1292805 seqs, 313927144 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Gaps

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     Relating To Prolactin Releasing Peptide (PrRP)
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Publication No US20020143152A1

GENERAL INCORMATION:

APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji

TITLE OF INVENTION: Polyeptides, their Production and Use
FILE REFERENCE: 2463US2P

CURRENT FILING DATE: 2002-01.10

PRIOR APPLICATION NUMBER: US 09/40339

PRIOR FILING DATE: 1999-25-10

PRIOR PILING DATE: 1998-04-27

PRIOR APPLICATION NUMBER: UF 1/7/JP98/01923

PRIOR FILING DATE: 1998-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    General INFORMATION Shuji
APPLICANT: Hintum, Shuji
APPLICANT: Fikusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463082P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-64-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                            Length 31;
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                                                                                                                                                                                                                                                                                                                                       99.4%; Score 168; DB 14; Length 3 100.0%; Pred. No. 1e-16; ive 0; Mismatches 0; Indels
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99.4%; Score 168; DB 13;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 30; Conservative 0; Mismatches 0;
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 14
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 90, Application US/10044592 Publication No. US20020143152A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 30; Conservative
                                                                                                                                                                                                                                            TYPE: PRT CRGANISM: Rattus US-10-096-777-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Rat
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US-10-044-592-90
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Fublication No. US20020143152A1

Fublication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use

FILE REPERENCE: 2463U525

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT APPLICATION NUMBER: US/2002-01-10

PRIOR FILING DATE: 1999-25-10

PRIOR FILING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: PCI/JP98/01923

PRIOR FILING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: PCI/JP98/01923

PRIOR PILING DATE: 1999-25-10

PRIOR PILING DATE: 1997-04-28

SOFTWARE:

SEQ ID NO S

LENGTH: 31

LENGTH: 31
TITLE OF INVENTION: Polypeptides, their Production and Use FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.4%; Score 168; DB 13; Length 31; Best Local Similarity 100.0%; Pred. No. 1e-16; Matches 30; Conservative 0; Mismatches 0; Indels
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US-10-096-777-14
US-10-096-777-14
Sequence 14, Application US/10096777
Publication No. US20030171270A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: antigen US-10-044-592-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Marches 30, Conservative
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                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Murine
US-10-044-592-4
                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                             LENGTH:
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APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods

Gaps .. 0

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NAME/KEY: misc feature
LOCATION: (1)...(31)
LOCATION: (1)...(31)
LOCATION: (925)...(955)
OTHER INFORMATION: primer
NAME/KEY: misc_feature
LOCATION: (1)...(955)
OTHER INFORMATION: insert fragment of pmGB3 as depicted in FIG 36 and 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

99.4%; Score 168; DB 13; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 30; Conservative 0; Mismatches 0; Indels
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APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2263US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR PRILING DATE: 1999-25-10
PRIOR PAPLICATION NUMBER: PCT/JP98/01923
PRIOR PILING DATE: 1998-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Civelli, Olivier
APPLICANT: Lin. Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For INTER OF INVENTION: Screening and Therapeutic Methods FOR INTER OF INVENTION: Promoting Wakefulness and Sleep FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
FRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 SKAHÓHSMETRIPDINPAWYIGRGIRPVGR 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 13, Application US/09932161; Patent No. US20020037533A1; GENERAL INFORMATION:
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Best Local Similarity 93.33
Matches 28; Conservative
  ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bos taurus
US-09-932-161-13
                                                                                                     TYPE: PRT
ORGANISM: Mammalian
NUMBER OF SEQ I
SOFTWARE:
SEQ ID NO 94
LENGTH: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-10-044-592-39
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                                                                                                                                                           FEATURE
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Sequence 96, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION

APPLICANT: Hinuma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use

TITLE OF INVENTION: Polypeptides, their Production and Use

TITLE OF INVENTION: Polypeptides, their Production and Use

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 2002-01-10

PRIOR APPLICATION NUMBER: US 09/403639

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE:
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| Sequence 94, Application US/10044592
| Publication No. US20020143152A1
| GENERAL INFORMATION:
| APPLICANT: Hinuma, Shuji
| APPLICANT: Fukusumi, Shoji
| TITLE OF INVENTION: POLYPeptides, their Production and Use FILE REFERENCE: 24631822P
| CURRENT APPLICATION NUMBER: US/10/044,592
| CURRENT FILING DATE: 1999-25-10
| PRIOR APPLICATION NUMBER: PCT/JP98/01923
| PRIOR FILING DATE: 1999-45-10
| PRIOR FILING DATE: 1999-45-10
| PRIOR FILING DATE: 1999-45-10
| PRIOR FILING DATE: 1999-74-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.4%; Score 168; DB 13; Length 86; 100.0%; Pred. No. 3.1e-16; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1224)..(1243)
OTHER INFORMATION: Bracket region depicted in FIG 39.
                                                                                                                                                                                                                                  Query Match 99.4%; Score 169; DB 13; Best Local Similarity 100.0%; Pred. No. 2.9e-16; Matches 30; Conservative 0; Mismatches 0;
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        PRIOR FILING DATE: 1997-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 30; Conservative
                                NUMBER OF SEQ ID NOS: 96
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: mammalian
                                                                                                                                   TYPE: PRT
ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-044-592-94
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LENGTH: 86
TYPE: PRT
                                                                                                                                                                                       US-10-044-592-1
                                                                               SEQ ID NO 1
LENGTH: 82
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DB 13;
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Pred. No. 4.1e-15;
                                                 Score 157; DB 13
Pred. No. 4e-15;
0; Mismatches
                                                                                                                                                                                        1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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                                                 92.9%;
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Best Local Similarity 93.3%;
Matches 28; Conservative (
                                               Query Match
Best Local Similarity 93.3
Matches 28; Conservative
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; ORGANISM: Bovine
US-10-044-592-41
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CRGANISM: Murine
US-10-044-592-28
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US-10-044-592-41
       US-10-044-592-40
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LENGTH: 98
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US-10-096-777-13

Sequence 13, Application US/10096777

Publication No. US20030171270A1

SEQUENCE 13, Publication No. US20030171270A1

SPELICANT: Civelli, Olivier

APPLICANT: Lin, Steven

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)

FILE REFERENCE: P-UC 3534

CURRENT APPLICATION NUMBER: US/10/096,777

CURRENT PILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: US/09/560,915

PRIOR APPLICATION NUMBER: US/09/560,915

NUMBER OF SEQ ID NOS: 24

SOFTWARE FILENCE DATE: 2000-04-28

NUMBER OF SEQ ID NO 13

LENGTH: 31
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US-10-044-592-40
sequence 40, Application US/10044592
sequence 40, Application US/100435241
septication No. US20020143152A1
septication Production and Use
TILLE OF.INVENTION: Polypeptides, their Production and Use
TILLE OF.INVENTION: Polypeptides, their Production and Use
STILLE OF.INVENTION: POLYPEPTION UNMER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR FILING DATE: 1999-28: US/403639
PRIOR FILING DATE: 1999-28: US/403639
PRIOR RELING DATE: 1999-24-7
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR RELING DATE: 1997-04-28
SOFTWARE:
SEQ ID NO 40
LENGTH: 32
munt ...
LENGTH: 32
LENGTH: 32
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                                                                                                                                                                                                                                                                                                                                                               1 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 30
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PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
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Best Local Similarity 93.3
Matches 28; Conservative
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ORGANISM: Bos taurus
                                                                                                                                         TYPE: PRT
CORGANISM: Bovine
US-10-044-592-39
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ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-096-777-13
                                                                   SOFTWARE:
SEQ ID NO 39
LENGTH: 31
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Best Local S:
Matches 28
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Bublication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REPERENCE: 2463U53D;

FILE REPERENCE: 2463U53D;

FILE REPERENCE: 2463U53D;

PRIOR APPLICATION NUMBER: US/10/044,592

CURRENT APPLICATION NUMBER: US/00/044,592

PRIOR PILING DATE: 1999-25-10

PRIOR RILING DATE: 1999-27

PRIOR APPLICATION NUMBER: PCT/J998/01923

PRIOR FILING DATE: 1999-27

NUMBER OF SEQ ID NOS: 96

SOFTWARE:

SEQ ID NO 41

LENGHIH: 33

TWOS: DATE: 133
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| Sequence 28, Application US/10044592
| Sequence 28, Application US/10044592
| Publication No US20020143152A1
| GENERAL INPORMATION:
| APPLICANT: Hinum, Shuji
| APPLICANT: Fikusumi, Shoji
| TITLE OF INVENTION: PolyPeptides, their Production and Use
| FILE REFERENCE: 24645022P
| CURRENT APPLICATION NUMBER: US/10/044,592
| CURRENT FILING DATE: 1999-25-10
| PRIOR FILING DATE: 1999-25-10
| PRIOR FILING DATE: 1998-04-27
| SOFTWARE:
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Length 32,
                                               2; Indels
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US-10-044-592-38
; Sequence 38, Application US/10044592
; Sequence 38, Application US/10044592
; Publication No. US20020143152A1
; GANERAL INFORMATION:
    APPLICAMT: Hunman, Shuji
    APPLICAMT: Fukusumi, Shoji
    TITLE OF INVENTION: Polypeptides, their Production and Use;
    FILE REFERENCE: 2463029
; FILE REFERENCE: 2463029
; FRICK RPLICATION NUMBER: US 09/403639
; PRIOR PLLING DATE: 1999-25-10
; PRIOR FILING DATE: 1999-25-10
; RIOR FILING DATE: 1997-04-28
; SEQ ID NO 38
; LENGRIER OF SEQ ID NOS: 96
; SOFTWARE:
; SEQ ID NO 38
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.9%; Score 157; DB 13; Length 98; Best Local Similarity 93.3%; Pred. No. 1.3e-14; Matches 28; Conservative 0; Mismatches 2; Indels
23 SRAHQHSMEIRTPDINPAWYAGRGIRPVGR 52
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99.4%; Score 168; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 9e-19;
Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Noriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Patent BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent IN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTOREY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
RELECOMMUNICATION INFORMATION:
TELEBRAX: 617-523-440
INPORMATION FOR EQUID NO: 8:
SEQUENCE CHRARACTERISTICS:
LENGTH: 31 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, 130 Water Street
              US-08-776-971-7
US-09-471-17
US-09-71-18
US-08-776-971-14
US-08-776-971-115
US-08-776-971-115
US-08-776-971-117
US-08-776-971-126
US-08-776-971-136
US-09-105-6788-29
US-09-105-6788-29
US-09-105-6788-29
US-09-105-6788-29
US-09-105-6788-29
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US-09-421-208-9
US-09-421-208-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 31 amino acids amino acid
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STREET: 130 Wa
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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US-09-105-678A-8
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Sequence 37, Appl
Sequence 4, Appli
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                                                                                                                                                        August 12, 2004, 14:37:36; Search time 17.6628 Seconds (without alignments) 90.609 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 137,
Sequence 7, A
Sequence 31,
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Sequence 39,
Sequence 49,
Sequence 39,
Sequence 39,
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Sequence 13,
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Sequence 6,
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                            SRAHQHSMETRTPDINPAWYTGRGIRPVGRX 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-105-678A-8
US-09-105-678A-8
US-09-172-35-4
US-09-172-35-4
US-09-411-208-8
US-09-411-208-8
US-09-56-915-14
US-09-95-95-4
US-09-105-678A-38
US-09-105-678A-38
US-09-105-678A-39
US-09-105-678A-39
US-09-105-678A-39
US-08-776-971-124
US-09-105-678A-39
US-08-776-971-137
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                       389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued Patents AA:*
                                                                                                                                                                                                                                       US-09-700-643A-3
169
1 SRAHQHSMETRIPDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match
                                                                                                                                                                                                                                                                         score:
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Maximum DB s
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Perfect
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No.
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us-09-700-643a-3.rai

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Kitada, Chieko
TITLE OF INVENTION: POLYPROFEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                               Query Match 99.4%; Score 168; DB 3; Length 31; Best Local Similarity 100.0%; Pred. No. 9e-19; Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT LIEM Compatible
CORRUTER: IBM Compatible
COERATING SYSTEM: DOS
SOFTWARE: FESTSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION AND BATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/0P96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 9/341371
FILING DATE: 12-MAR-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                               1 SRAHOHSMETRIPDINPAWYTGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
NOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-08-776-971-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%; Score 168;
                                                                                                                                                                                                                                                                                                                                                              Sequence 47, Application US/08776971B
Patent No. 622898
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukusumi,
                         ) ORGANISM: Mus musculus US-09-172-353-4
                                                                                                                                                                                                                                                                                                                                       -08-776-971-47
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Patent No. 6197530
GENERAL INFORMATION:
APPLICANT: Stricker-Kongra, Alain
APPLICANT: Gu, Wei
TITLE OF INVENTION: GPRIO AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS
FILE REPERENCE: 07334/102001
CURRENT APPLICATION NUMBER: US/09/172,353
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 4
LENGTH: 31
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                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Stenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
IITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 5.2
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
1 SRAHQHSMETRTPDINPAWYTGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SRAHQHSMETRTPDINPAWYTGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                          Sequence 37, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COLLIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
                                                                                                                    US-09-105-678A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-172-353-4
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168; DB 3; Length 31;
No. 9e-19;
                METHOD OF PRODUCING A 19P2 LIGAND
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208
FILING DATE:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:

NAME: COALIN, David G.

REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 27,026
REPRENCE/DOCKET NUMBER: 27,026
REPR
      NUMBER OF SEQUENCES: 52
CORRESPONDENCE 52
CORRESPONDENCE 5DRESS: 52
CORRESPONDENCE ADDRESS: 52
STREET: 130 Water Street
CITY: Boston
STREET: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
99.4%; Score 168; DE
Best Local Similarity 100.0%; Pred. No. 9e-
Matches 30; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-09-560-915-14
'Sequence 14, Application US/09560915
'Patent No. 6383764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 31 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-421-208-37
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; ORGANISM: Rattus
US-09-560-915-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                   ZIP: 02109
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LENGTH: 31
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Sequence 8, Application US/09421208;
Patent No. 625851;
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.4%; Score 168; DB 3; Length 31; Best Local Similarity 100.0%; Pred. No. 9e-19; Matches 30; Conservative 0; Mismatches 0; Indels
Pred. No. 9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION.DATA:
APPLICATION NUMBER: US/09/421,208
            100.0%; Prec. ....
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                                                                                                                    1 SRAHQHSMETRTPDINPAWYTGRGIRPVGR 30
                                                                                                                                                                     1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 26-UNN 1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UNN 1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIA, DAA'IS G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIF: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suenaga, Masato
Moriya, Takeo
Tanaka, Yoko
Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 amino acids
                             Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -09-421-208-37
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US-09-421-208-8
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

APPLICANT: Lin, Steven

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)

FILE REFERENCE: P-UC 3534

CURRENT APPLICATION NUMBER: US/09/560,915

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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Gaps
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
                                                                                                                    Length 32;
                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                               Score 168; DB 3; I
Pred. No. 9.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B
TLASSIFICATION **CURRENT APPLICATION NUMBER: US/08/776,971B
TLASSIFICATION **CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: UP 1/34371
FILING DATE: 18-DEC-1995
APPLICATION NUMBER: UP 8/59419
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: UP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: UP 8/211805
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: COALIN, DAVIG G
REPERENE/DOCKET NUMBER: 27,026
RECISTRATION NUMBER: 27,026
                                                                                                                 99.4%; Score 168; DB ilarity 100.0%; Pred. No. 9.4 Conservative 0; Mismatches
                                                                                                                                                                                                                                                    1 SRAHQHSMETRTPDINPAWYTGRGIRPVGR 30
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MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                   Sequence 48, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hinuma, Shuji
Habata, Yugo
                          TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-105-678A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                     Query Match
Best Local Similarity
Matches 30, Conserv
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US-08-776-971-48
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                                                                                           Sequence 4, Application US/09799955
Patent No. 6537765
GENERAL INFORMATION:
APPLICANT: Stricker-Kongra, Alain
APPLICANT: GL, Wei
TITLE OF INVENTION: GPA10 AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS
FILE REFERENCE: 07334/102001
CURRENT APPLICATION NUMBER: US/09/799,955
PRIOR PAPLICATION NUMBER: US/09/712,353
PRIOR PILING DATE: 1996-10-14
NUMBER OF SEQ ID NOS: 7
SEQ ID NOS: 7
LENGTH: 31
LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 122118/1997
ATTORNEY/AGENT INFORMATION:
1 SRAHQHSMETRTPDINPAWYTGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SRAHQHSMETRTPDINPAWYTGRGIRPVGR 30
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REGISTRATION NUMBER: 27,026
REFRENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 38:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONG
STREET: 130 Water Stre
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mus musculus
US-09-799-955-4
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US-09-105-678A-38
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Gaps
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.4%; Score 168; DB 3; Length 33; Best Local Similarity 100.0%; Pred. No. 9.7e-19; Matches 30; Conservative 0; Mismatches 0; Indels
              TITE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLF STREET: 130 Water Street
STREET: Boston
STATE: MA
COUNTRY: UGA
CIPY: LO2109
                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: UP 172118/1997
PRIOR APPLICATION NUMBER: JP 172118/1997
PRIOR APPLICATION NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REGISTRATION NUMBER: 27.026
REFERENCE/DOCKET NUMBER: 27.026
REJERPHONE: 617-523-3400
FILIEFRAM: 617-523-3400
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OPERATING SYSTEM: DOS
SOFFWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SRAHQHSMETRTPDINPAWYTGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hinuma, Shuji
Nishimura, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-105-678A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-08-776-971-49
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
   Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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ZIP: 02109

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 168; DB 3; I
100.0%; Pred. No. 9.4e-19;
tive 0; Mismatches 0;
       DB 3; I
9.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
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   Query Match
99.4%; Score 168; DE
Best Local Similarity 100.0%; Pred. No. 9.4
Matches 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION MOMBER: US 09/105,678
FILING DATE: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 25-UN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTILIN, DAVIG G.
REFIRENCE/DOCKET NUMBER: 48466-342
FELESCOMMUNICATION INFORMATION:
TELEPROCE/ONCET NUMBER: 48466-342
FELECOMMUNICATION INFORMATION:
TELEPROCE/ONCET NUMBER: 48466-342
FELEPROCE/ONCET NUMBER: 48466-342
FELEPROCET NUMBER: 48466-342
FELEPROCET NUMBER: 617-523-6440
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                         1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
                                                                                                                                                                                                      1 SRAHOHSMETRIPDINPAWYTGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-421-208-38
; Sequence 38; Application US/09421208
; Patent No. 628561
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Best Local Similarity 100.
Matches 30; Conservative
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; MOLECULE TYPE: peptide
US-09-421-208-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-105-678A-39
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US-08-776-971-45

| Sequence 45, Application US/08776971B |
| Sequence 45, Application US/08776971B |
| Sequence No. 6.28984 |
| GENERAL INFORMATION: Hinuma, Shuji |
| APPLICANT: Hinuma, Yuji |
| Rawamata, Yuji |
| Habata, Yugo |
| Kawamata, Yuji |
| Fujii, Roya, Masaki |
| Fujii, Roya, Masaki |
| Fujii, Roya, PolyPROTEINS, THEIR PRODUCTION AND USE |
| NUMBER OF SEQUENCES: 140 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: DIES, BRONSTEIN, ROBERTS & CUSHMAN, LLP |
| STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                            99.4%; Score 168; DB 3; Length 33; 100.0%; Pred. No. 9.7e-19; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: PESTESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
PILING DATE: 06-Feb-1997
CLASSIFICATION: AUNGER: US/08/776,971B
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/34371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AQ1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRAHQHSMETRIPDINPAWYTGRGIRPVGR 30
              REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 animo acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 45
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 30; Conservative
Conlin, David G.
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                          US-09-421-208-39
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1 Similarity 100.0%; Pred, No. 9.7e-19;
30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/09421208
Patent No. 6258561
GENERAL. INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTE PC_DOS/MS_DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/421,208 FILING DATE:
                 CLASSIFICATION: CUILALO....

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 9/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/211805
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/21636
APPLICATION NUMBER: JP 8/21636
ATTORNEY/AGENT INFORMATION:
NAME: CONIIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUICATION INFORMATION:
TELEPRONE: 617-523-3400
TELEPRAX: 617-523-5440
TELEPRAX: 617-523-5440
TELEPRAX: 617-523-5440
TELEPRAX: 617-523-5440
TELEPRAX: 617-523-5440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SRAHQHSMETRTPDINPAWYTGRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLGGY: linear
MOLECULE TYPE: protein
FRAGWRNT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
              FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Flogby disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTMARE: Patenty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: DIKE, BRONSTE
130 Water Street
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match .
Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-421-208-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-776-971-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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us-09-700-643a-3.rai
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SEQUENCE CHARACTERISTICS:

IENGTH: 83 amino acids

TYPE: amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-08-776-971-45

Query Match

Best Local Similarity 100.0%; Pred: No. 2.9e-18;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps

Oy ISRAHOHSMETRTPDINPAWYTGRGIRPVGR 30

Db 22 SRAHQHSMETRTPDINPAWYTGRGIRPVGR 51

Search Completed: August 12, 2004, 14:52:13

Job time: 17.6628 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

August 12, 2004, 14:37:36; Search time 8.83721 Seconds (without alignments) 217.697 Million cell updates/sec Run on:

US-09-700-643A-5

108 1 TPDINPAWYASRGIRPVGRX 20 Perfect score: Sequence: BLOSUM62 Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

nitrite extrusion	xanthine dehydroge	xanthine dehydroge	N-acetylglutamate	hypothetical prote	protein-export mem	transcription regu	hypothetical prote	probable transcrip	hypothetical prote	cytochrome-c oxida	LytB homolog [impo				
C83160	T10235	T10236	D84012	T19997	A97505	AE2723	A12484	S76955	B82824	H82608	H84584	A75366	G7560B	266600	E87151
N	N	~	~1	0	~	N	(7)	N	N	N	N	C)	N	N	N
468	1359	1364	345	3944	105	105	113	128	132	216	219	221	232	311	335
39.8	39.8	39.8	39.4	39.4	38.9	38.9	38.9	38.9	38.9	38.9	38.9	38.9	38.9	38.9	38.9
43	43	43	42.5	42.5	42	42	42	42	42	42	4.2	42	42	42	42

ALIGNMENTS

C; Species: Rattus norvegicus (Norway rat)
C; Species: Jo-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C; Accession: JG7607
R; Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T.
B; Jachem. Bloghya. Res. Commun. 281, 53-56, 2001
A; Title: Isolation and characterization of the rat prolactin-releasing peptide gene: Mul
A; Reference number: JG7607; MUID:21092785; PMID:11178959
A; Rointer: Spleen
A; Accession: JG7607
A; Molecule type: DNA
A; Content: Spleen
A; Molecule type: DNA
A; Residues: 1-83 ** YAMA
A; Conson: Teferences: DDBJ:AB040612; DDBJ:AB040613
C; Comment: This peptide induces arachidonic acid metabolite release from rat anterior prolatese, and stimulation of ACTH secretion from the pituitary.
C; Genetics:
A; Genetics:
A; Genetics:
A; Christons: 33/1

Gaps , 0 Length 83; 91.7%; Score 99; DB 2; Length 83; 89.5%; Pred. No. 2.3e-08; ative 0; Mismatches 2; Indels 0; Query Match
Best Local Similarity 89.5
Matches 17, Conservative

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hypothetical protein F15G16.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47959
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet Submitted to the Protein Sequence Database, January 2000
A;Reference number: Z24480
A;Accession: T47959

A;Map position: 3 A;Introns: 39/1; 678/2; 698/3; 773/2 A;Note: F15G16.60

Length 790; DB 2; Score 53; DB : Pred. No. 3.4; 49.1%; 55.6%; Query Match Best Local Similarity N

366 PPHNPRTYGSRGLOPHGR 383

?

Matches

à g

19

PDINPAWYASRGIRPVGR 10; Conservative

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CiACCESSION HEALD:
CiACCESSION: HEALD:
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CiACCESSION: HEALD:
CiACCESSION: HEALD:
Nature 406, 151-157, 2000
A,Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Reference number: A82515; MUID: 20365717; PMID: 10910347
A,Note: for a complete list of authors see reference number A59328 below
A,Accession: H82652
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-333 <SIM>ASIM>ARESIMA
A,Residues: 1-333 <SIM>ASIM>ARESIMA
A,Residues: 1-333 <SIM>ASIM>ARESIMA
A,Residues: L-333 <SIM>ASIM>AREMANOI.
A,Gross-references: GB: AFRO03860; GB: AB003849; NID: G9104830; PIDN: AAFR2881.1; GSPDB: GN001.
A,Experimental source: strain 935C
A,Experimental source: strain 935C
A,Experimental source: strain 945C
A,A.; Ferno, A.A.; Ferno, A.A.; Camrargo, A.J.; Fernora, A.J.; Marchors, Martins, E.M.; Matchors: Martins, E.M.; Matchors: Martins, E.M.; M.; Matchors, M.; Silva Jr.; Mayaki, C.F.; A,Authors: da Silva, A.J.; de Rosa Jr., V.E.; de Oliveira, R.J.; Advasaki
A,Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr.; MA.; Silva Jr.; MA.; A,Authors: da Silva, A.J.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypotherical protein At2g06860 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: C84480
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. R; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., Buss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84480
A;Accession: C84480
A;Accession: Drawnary
A;Residues: 1-988 eSTO.
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Pred. No. 35;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: 4-hydroxybenzoate octaprenyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 2;
Pred. No. 12;
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53.3%;
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Matches 10; Conservative
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nes 8; Conserv
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C, Accession: H82852
R, anonymous, The XV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: XF0068
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P71015

hypochetical protein PH1420 - Pyrococcus horikoshii

C; Species: Pyrococcus horikoshi
C; Species: Pyrococcus horikoshii
C; Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C; Accession: P71015

R; Kawarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
R; Kawarabayasi, Y; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA R; S5-76, 1998
A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A; Reference number: A71000; WUID:98344137; PMID:9679194
A; Reference number: A71000; WUID:98344137; PMID:9679194
A; Reference number: A71000; MID:3236133; PIDN:BAA30526.1; PID:g3257843
A; Roses:references: GB:Ap000006; NID:g3236133; PIDN:BAA30526.1; PID:g3257843
A; Crose-references: GB:Apococcus ninterim accession for a sequence replaced by GenBank
C; Genetics:
A; Gene: PH1420
C; Superfamily: Pyrococcus horikoshii hypothetical protein PH1420
                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein PA2151 [imported] - Peeudomonas aeruginosa (strain PA01) (Species: Peeudomonas aeruginosa (Species: Peeudomonas aeruginosa (Species: Peeudomonas aeruginosa (Species: Peeudomonas aeruginosa (Space: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 (Spacession: F83376 PS376 PS377 PMID:10984043 PA01, an opportunistic patholystatus: preliminary PS376 PS377 PMID:10984043 PS376 PS376 PS376 PS376 PS376 PS376 PS377 PMID:10984043 PS376 
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H82852
hydroxybenzoate octaprenyltransferase XF0068 [imported] - Xylella fastidiosa (strain 9a5 C; Species: Xylella fastidiosa (strain 9a5 C; Species: Xylella fastidiosa C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN001
A;Expertimental source: strain PA01
C;Genetics:
A;Gene: PA2151
          ö
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Pred. No. 10;
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          Indels
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          9
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46.8%; Score 50.5; DE
Best Local Similarity 62.5%; Pred. No. 6.9;
Matches 10; Conservative 1; Mismatches
          Mismatches
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TPDINP-WFLORSGRP 492 1 TPDINPAWYASRGIRP 16

g 8

1-664 <STO>

234

2 PDINPAWYASRGIRPVGR 19

217 PYIEPTFYALRGLELLGR

g

Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative

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A;Cross-references: 1-370 told)
A;Cross-references: GB:AE003866; GB:AE003849; NID:g9104906; PIDN:AAF82941.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.B.; Camargo, L.E.A.; Carraro, D.M.; Carrer, B Briones, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, B submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.P.; Franca, S.C.; Franco, M.C.; Frohr J.D.; Junqueira, W.C.A.; Ferro, J.A.; Fraga, J.P.; Krieger, J.E.; Kiraima, W.C.; Frohr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitaima, J.P.; Krieger, J.E.; Kiramae, E.E.; Lasgr Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.A.; Authors: M. Marchia, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Aluthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.R.; Verference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conserved hypothetical protein MTH1070 - Methanobacterium thermoautotrophicum (strain Dc C,Species: Methanobacterium thermoautotrophicum C,Species: Methanobacterium thermoautotrophicum C,Species: Methanobacterium thermoautotrophicum C,Species: Jo-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 23-Jul-1999 C,Accession: B69009 C,Accession: B69009 R,Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Alu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
J. Hance Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A,Reference number: A69000; MUID:98037514; PMID:9371463
A,Accession: B69009
A,Accession: B69009
A,Residues: 1-430 AMTH>
A,Residues: 1-430 AMTH>
A,Residues: 1-430 AMTH>
A,Residues: 1-430 AMTH>
A,Residues: Leferences: GB,AE000877; GB:AE000666; NID:g2622157; PIDN:AAB85559.1; PID:g262216
A,Experimental source: strain Delta H
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hypothetical protein F38E11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: IS-Oct-1999 #sequence_revision IS-Oct-1999 #text_change IS-Oct-1999
C;Accession: T21969
R;Matthews, P.
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Pred. No. 32;
0; Mismatches 5; Indels
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C,Superfamily: conserved hypothetical protein MTH1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 2;
Pred. No. 29;
2; Mismatches
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61.5%;
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Best Local Similarity 70.07
Fest Local 7; Conservative
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354 SPAWYAAHGI 363
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Best Local Similarity
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B69009
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C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G82844
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
N,Alternate names: protein B23L21.300
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49717
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Reference number: Z25022
A;Accession: T49717
A;Status: preliminary
A;Accession: L47917
A;Residues: 1-779 < CCH>
A;Accession: BAC Clone B23L21; strain OR74A
A;Residues: 1-779 < CCH>
A;Coss-references: EMBL:AL356172; GSPDB:GN00116; NCSP:B23L21.300
C;Genetics: A;Genetics: A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypotherical protein ugpB [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pl C; Species: Agrobacterium tumefaciens C; Accession: AH3166
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ster, E.W.
A,TILle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Ritle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AB3166
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1419 <KUR>
A,Residues: 1419 <KUR>
A,Ecoss-references: GB:AE008687; PIDN:AAL45750.1; PID:g17743483; GSPDB:GN00188
A,Experimental source: strain C58 (Dupont)
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22;
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
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A;Genome: plasmid
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8 В

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hypothetical protein Rv0428c - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Accession: B76631
R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Ghurcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Parkhill, J.; Seger, K.; Skelton, S.; Aguares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A.Authors: Saares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Authors: Saares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Reference number: A70500; MUID:98295987; PMID:9634230
A.Reference number: A70500; MUID:98295987; PMID:9634230
A.Molecule type: DNA
A.Residues: 1-302 cCOL>
A.FEXperimental source: strain H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF025462; PIDN:AAB71002.1; GSPDB:GN00021; CESP:K10F12.4
A;Experimental source: strain Bristol N2; clone K10F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein K10F12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T2376
R;Wohldmann, P.; Beck, C.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid K10F12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,cene: Rv0428c
C,Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0428c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 2; Length 302;
Pred. No. 32;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
40.7%; Score 44; DB 2;
Best Local Similarity 44.4%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches
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he : 8.83721 secs
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A;Introns: 31/3; 123/2; 196/3; 239/1
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      217 PYIEPTFYALRGLELLGK 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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126 AWYASRDLQP 135
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Job time :
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A75117

Pypothetical protein PAB0502 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C;Accession: A75117

R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru

A;Reference number: A75001

A;Status: preliminary
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A.Molecule type: DNA
A.Residues: 1-284 «KAW>
A.Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49650.1; PID:g545816
A.Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL022003; GB:AL123456; NID:g3261547; PIDN:CAA17613.1; PID:g326154
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cipence in Mycobacterium tuberculosis
Cipate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
Cipate: 18-Jul-1998 #sequence in T. Gartles, S.; Hamin, N.; Holroyd, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamin, N.; Holroyd, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: D70817
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                A;Gene: CESP:F38E11.7
A;Map position: 4
A;Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1;
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A,Cross-references: EMBL:Z68342; PIDN:CAA92775.1; GSPDB:GN00022; CESP:F38E11.7 A,Experimental source: clone F38E11
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D70817
hypothetical protein Rv1716 - Mycobacterium tuberculosis (strain H37RV)
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111 TPDIRPGDIVVVNTGWHHKYADSAEYYAYSPGFDKKAGEWFAAKGVKAVG 160
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C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1420
                                                                                                                                                                                                                                 Score 45; DB 2; Length 767;
Pred. No. 58;
1; Mismatches 1; Indels
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Pred. No. 29;
5; Mismatches 3; Indels
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Pred. No. 30;
4; Mismatches 6; Indels
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 20.0%;
Matches 10; Conservative
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Best Local Similarity 44.4%;
Matches 8; Conservative
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Gene: PAB0502
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RESULT 13

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PDINPAWYASRGIRPVGR 19

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2004, 14:37:35; Search time 5.23256 Seconds (without alignments) 199.024 Million cell updates/sec Run on:

US-09-700-643A-5 108 1 TPDINPAWYASRGIRPVGRX 20 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	81277	81264 bos t	P81278 rattus norv	9fbm3	U			P30143 escherichia		Q37893 bacteriopha		P35360 limulus pol	P35361 limulus pol	Q82jf0 streptomyce							akr		-			-	_	P29978 anabaena sp	rattr		рошо	arbac	bovine a	
SUMMARIES	ID	RP	PRRP_BOVIN	PRRP_RAT	EX7L_STRCO	CYCR_CHRVI		EX7L_CORGL	YAAJ_ECOLI	NRP1_YEAST	VG12_BPB03	GIDB_PSESM	OPS1_LIMPO	OPS2_LIMPO		ARGC BACHD	ISPH_MYCLE	YAIW ECOLI	HMT2_SCHPO	UBP3_SCHPO	POL MLVRK	POL_MLVAK	POPC_RALSO	POL MLVAV	POL_MLVRD	RIF1_SCHPO	Y762_METJA		YE48 ANASP		EXL1_HUMAN	LCFF HUMAN	CYGR_ARBPU	HEX8_ADEB2	
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Q9yf98 aeropyrum p P34347 caenorhabdi Q9nvr5 homo sapien P23832 salmonella P11292 woodchuck h P21316 saccharomyc Q86da5 pseudomonas Q8caq8 mus musculu P44408 haemophilus Q9pfd6 xylella fas Q87ab6 xylella fas P03160 woodchuck h
RL15 AERPE YK69 CAEBL CNA4 HUMAN SAMB SALTY DPOL WHVW6 ATHUC PERPK INNT MOUSE RECZ HAEIN SYFB XYLFA SYFB XYLFA BPOL WHV1
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# ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
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Mature 393:272-276(1998).

-! FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin hrough its receptor GPR10. May stimulate lactorophs directly to secrete PRL.

-! TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MXY-2000 (Rel. 39, Created)
30-MXY-2000 (Rel. 39, Last sequence update)
30-MXY-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDATION (G-54 PROVIDE AMIDE GROUP)
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PROLACTIN-RELEASING PEPTIDE PRRP20.
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Hormone, Amidation, Signal, Cleavage on pair of basic residues.
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0
Query Match

99.1%; Score 107; DB 1; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 19; Conservative 0; Mismatches 0; Indels
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PRRP RAT
AC P81278; Q8K3Y0; PRT; 83 AA.
AC P81278; Q8K3Y0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             98 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98268781; PubMed=9607765;
                                                                                                                                               1 TPDINPAWYASRGIRPVGR 19
                                                                                                                                                                                                                34 TPDINPAWYASRGIRPVGR 52
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98 AA; 10544 MW;
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AC 30-MAY-2000
DT 30-MAY-2000
DT 30-MAY-2000
DT 30-MAY-2000
DT 30-MAY-2000
DT 30-MAY-2000
DF ACTORNEY
CO BE CONTROLLINE
CO BOX HOLE
CO CO CO BOX HOLE
CO BOX HOL
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                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSUE=Hypothalamus;
Anderson S.T., Kokay I.C., Lang T., Grattan D.R., Curlewis J.D.;
Auduntitation of prolactin-releasing peptide (PPRP) mRNA expression in specific brain regions during the rat oestrous cycle and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION (G-53 PROVIDE AMIDE GROUP).
TPDINPAWYTGRGIRPVGRFGRRRATPRDVTGLGQLSCLPL
DGRTKFSQRG -> SECLTYGKQPLTSFHPFTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ul. Pept. 83:1-10(1999).
FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
ALTERNATIVE PRODUCTS:
                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                  MEDLINE 39268781; PubMed=9607765; Hindma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.; Marolactin-releasing peptide in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99426652; PubMed=10498338; Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sekiguchi M., Fujino M.; Fujino M.; Tissue distribution of prolactin-releasing peptide (PrRP) and its
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP20].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isold=P81278-2; Sequence=VSP_004370; TISSUE SPECIFICITY: Widely expressed, with highest levels in medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF521930; AAM82154.1; -.
PIR; JC7607; JC7607.
Hormone; Amidation; Signal; Cleavage on pair of basic residues;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP 004370.
D0C75A264EEE4F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P81278-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoform 2).
                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2).
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative splicing.
SIGNAL
22
SEGNAL
22
SEPTIDE 33
SEPTIDE 37
SROPEP 57
SAMOD_RES 52
VARSPLIC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PISSUE SPECIFICITY.
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                                                                                                                                  NCBL_TaxID=10116;
                                                                                                                                                                                            TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                          lactation."
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Matches
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                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2) / M145,
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
&
                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (BC 3.1.11.6)
                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 1; Length 402;
Pred. No. 5.1;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Nuclease; Exonuclease; Complete proteome.
SEQUENCE 402 AA; 43882 MW; 145929A8372B4E08 CRC64;
                                                                                                                 402 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL939122; CAC05901.1; -.
HAMAP; MF_00378; -; 1.
InterPro; IPR00353; Exonuc VII_L.
InterPro; IPR004365; tRNA_anti.
Pfam; PP01336; tRNA_anti; 1.
TIGRFAMS; TIGR00237; xseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEWYAPRGOLSLRAAEIKPVG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 PAWYASRG-----IRPVG 18
                        33 TPDINPAWYTGRGIRPVGR 51
1 TPDINPAWYASRGIRPVGR 19
                                                                                                                                                                                                              (Exonuclease VII large subunit)
XSEA OR SCO5056 OR SCK7.29C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                               Streptomyces coelicolor.
                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

COTSON G.E., Nagashima K.V., Matsuura K., Sakuragi Y., Ruwanthi W.,
COTSON G.E., Nagashima K.V., Matsuura K., Sakuragi Y., Ruwanthi W.,
Oin H., Allen R., Knaff D.E.,
T. The structure of genes encoding light-harvesting and reaction
center proteins from Chromatium vincsum.",
T. Submitted (MAR-1998) to the FWEL/GenBank/DDB databases.
C. --- FUNCTION: THE REACTION CENTER OF PURPLE BACTERIA CONTAIN A
TIGHTY BOUND CYTOCHROME MOLECULE WHICH RE-REDUCES THE PHOTO
OXIDIZED PRIMARY ELECTRON DONOR.
C.--- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(By similarity).
C.--- PTW: Binds 4 heme groups per molecule.
C.--- PTM: Binds 4 heme groups per molecule.
C.--- SIMILARITY: HIGH, WITH OTHER PHOTOSYNTHETIC REACTION CENTER
CYTOCHROME C SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNIT.
S-diacylglycerol cysteine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electron transport; Photosynthesis; Reaction center; Heme; Membrane;
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IRON (HEME 1 AXIAL LIGAND)
(BY SIMILARITY).
HEME 1 (COVALENT) (BY SIMILARITY).
HEME 1 (COVALENT) (BY SIMILARITY).
IRON (HEME 1 AXIAL LIGAND)
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(BY SIMILARITY)
                                                                                                                                Photosynthetic reaction center cytochrome C subunit precursor
                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales,
Chromatiaceae, Allochromatium.
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IRON (HEME 2 AXIAL LIGAND)
(BY SIMILARITY).
IRON (HEME 4 AXIAL LIGAND)
(BY SIMILARITY).
(BY SIMILARITY).
HEME 2 (COVALENT) (BY SIMILARIEM)
HEME 2 (COVALENT) (BY SIMILARIEM)
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IRON (HEME 3 AXIAL LIGAND)
(BY SIMILARITY).
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                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
  383 AA.
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HSSP; P07173; GPRC.
InterPro; IPR000345; CytC.heme_BS.
InterPro; IPR000345; CytC.RC.
Pfam; PF02276; CytoC_RC, T.
ProBom; PRRSPCO0017; RC_cytochrome; 1.
ProBom; PD010011; CytC_RC; 1.
PROSITE; PS00190; CYTOCHROME_C; 4.
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SIGNAL 1 22 BY SIMILAI
PRT;
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  STANDARD;
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                                                                                                                                                                                 Chromatium vinosum.
                                                                                                                                                                                                                                                          NCBI_TaxID=1049;
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  CHRVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 13:1572-1579(2003).

-!- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity).

-!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'- or 3'- to 5'-direction to yield nucleoside 5'-phosphates.

-!- SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                  HEME 4 (COVALENT) (BY SIMILARITY).
HEME 4 (COVALENT) (BY SIMILARITY).
IRON (HEME 4 AXIAL LIGAND)
                                                                                                                                                                                                                     ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura B., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.6%; Score 46; DB 1; Length 413; Best Local Similarity 52.4%; Pred. No. 7.6; Matches 11; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                    Score 46; DB 1; Length 383; Pred. No. 7;
                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the xseA family.
                                                                                                                     96BCD91FF1B9AE7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Nuclease; Exonuclease; Complete proteome. SEQUENCE 413 AA; 45171 MW; D3BABD9687C6EE5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                           413 AA
                                                                                             (BY SIMILARITY
                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00378; -; 1.
InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR008994; Nucleic_acid_OB.
Pfam; PF02601; Exonuc_VII_L; 1.
TIGRFAMS; TIGR00237; xseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP005217; BAC17888.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Exonuclease VII large subunit).
                                                                                                                                                                                                                                                                                                                   263 TPORTTAWYAIRHVRDING 281
                                                                                                                                                                                                                                                                    1 TPDINPAWYASRGIRPVGR 19
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10-OCT-2003 (Rel. 42, Last sequ
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                     383 AA; 41522 MW;
                                                                                                                                                                      42.68;
                                                                                                                                                                                                 42.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium efficiens,
                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                    307
                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=152794;
                       307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSEA OR CE1078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   efficiens.";
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Q8FQP1;
                                                                                                                     SEQUENCE
                    BINDING
BINDING
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
m
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28-FEB-2003 (Rel. 41, Last sequence update)
41. Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
                                                                                                                                                                                                                                                                               Corynebarterium glutamicum (Brevibacterium flavum).
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.6%; Score 46; DB 1; Length 417; 52.4%; Pred. No. 7.6; 1; Indels ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the xseA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase, Nuclease, Exonuclease, Complete proteome. SEQUENCE 417 AA; 45582 MW; B32CD9286C173C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                      417 AA
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAWAP; MF_00378; -; 1.
InterPro; IPR003753; Exonuc_VII_L.
InterPro; IPR008994; Nucleic_acid_OB.
Pfam; PF02601; Exonuc_VII_L; 1.
TIGRFAMS; TIGR00237; X86A; 1.
                                                                                                          PRT;
90 PAFYAGRGSFSLWVTDIRPVG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 PAFYAGRGTFSLWVTDIRPVG 114
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                                                                                                                                                                                                                                          (Exonuclease VII large subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP005277; BAB98418.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative transporter yaad.
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                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1718;
                                                                                                                                                                                                                                                               XSEA OR CGL1025
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ID YAAJ_ECOLI
AC P30143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia
                                                                                                        EX7L CORGL
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                                                                   RESULT
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6 PAWYASRG-----IRPVG 18

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                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pohl T.M.; (NOV-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1995) to the EMBL/CenBank/DDBJ databases.
-!- SIMILARITY: Contains 2 RANBP2-type zinc fingers.
-!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                              MEDLINE-93247548; PubMed-8483449;
Wehner E.P., Rao E., Brendel M.;
"Molecular structure and genetic regulation of SFA, a gene
responsible for resistance to formaldehyde in Saccharomyces
cerevisiae, and characterization of its protein product.";
Mol. Gen. Genet. 237:351-358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> N (IN REF. 1).
ADA9BC09FD582669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1,
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1988 (Rel. 37, Last annotation update)
Pre-neck appendage protein (Late protein GPI2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  860 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X68020; CAA48159.1; -.
EMBL, 267750; CAA91579.1; -.
EMBL, 274215; CAA9141.1; -.
PIR, 561046; S61046.
GermChline; 140410; -.
GGD, S0002326; NRP1.
InterPro; IPR001876; Znf_RanGDP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
      ARPI OR ARP OR YDL167C
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244 SWFTQYGVRPVG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AWYASRGIRPVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               719
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VG12_BBB03
ID_VG12_BBB03
AC_Q37893,
DT_15-DEC-1998
DT_15-DEC-1998
DT_15-DEC-1998
GN_12-neck app
GN_12-neck app
GN_12-neck app
GN_12-neck app
                                                                                                                                                                                                                                      STRAIN=AH22
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                                                                                                                                                                                                   SEQUENCE
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      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAINERIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-! SURCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                   οĘ
                                                                                                                          Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.; Systematic sequencing of the Escherichia coli genome: analysis the 0-2.4 min region...; Nucleic Acids Res. 20:3308-3308 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000111; AAC73118.1; -.

PIR; (64720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 664720; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (potential).
-!- SIMILARITY: BELONGS TO THE SODIUM ALANINE SYMPORTER FAMILY (SAF). STRONG, TO H.INFLUENZAE HIO183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
2F6EB2E12E126E63 CRC64;
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                                                              STRAIN=K12;
MEDLINE=92334977; PubMed=1630901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 DVNGQFRGGPAWYMARGL 137
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TRANSWEM 4 24
TRANSWEM 81 101
TRANSWEM 141 161
TRANSWEM 174 194
TRANSWEM 207 227
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300
351
391
414
476 AA;
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Best Local Similarity
[1]
SEQUENCE FROM N.A.
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RESULT 9 NRP1 YEAST

Best Loc Matches

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Length 719;

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EMBL; L03791; AAA28273.1; -.
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                                                                                                                                                                                                                                                                                        42.98;
                                                                                                                                                                                                                                                                                                                                                                                                        161 DVNTRWLAMKGLHP 174
                                                                                                                                                                                                                                                                                                                                                           3 DINPAWYASRGIRP 16
                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lateral eye;
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPS1 LIMPO
P35360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
OPS1_LIMPO
                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the butopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
A Gwinn M.L., Dodscon R.J., Deboy R.T., Durkin A.S., Kolonay J.F.,
A Madpu R., Daudherty S., Brinkac L., Beanan M.J., Haft D.H.,
A Nelson W.C., Davidsen T.Y., Zafar N., Zhou L., Liu J., Yuan Q.,
Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T.,
A Nan Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.L., Ramos A.R.,
A Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P.,
A Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,
Mitte O., Fraser C.M., Collmer A.,
The complete genome sequence of the Arabidopsis and tomato pathogen
Pseudomonas syringae pv. tomato DC3000.";
Proc. Natl. Acad. Sci. Us.A. 100:1081-10186 (2003).
C.-i- FUNCTION: Probable S-adenosyl-L-methionine dependent
methyltransferase specific for a sterol and/or lipid substrate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  no RNA stage; Caudovirales; Podoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Methyltransferase gidB (EC 2.1.-.-) (Glucose inhibited division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                              MEDIINE=98019084; PubMed=9358052; Pecenkova T., Benes V., Paces J., Vlcek C., Paces V.; Pacteriophage B103: complete DNA sequence of its genome and Terlationship to other Bacillus phages."; Gene 199:157-163(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         860 AA; 91741 MW; AC5B38F4BC65ECB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43.5; DB 1;
Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
SIMILARITY: Belongs to the gidB family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DC3000;
MEDLINE=22834015; PubMed=12928499;
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                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X99260; CAA67660.1; -.
InterPro; IPR006626; PbH1.
SMART; SM00710; PbH1; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
  viruses,
Viruses; dsDNA virus
phi-29-like viruses.
NCBL_TaxID=10778;
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                                                                                          SEQUENCE FROM N.A.
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GIDB OR PSPTO5609.
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SEQUENCE 86
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GIDB_PSESM
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42111 MW;
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                                                                                                                                                                                                                                                           Local Similarity 46.2
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                         193
376 AA;
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239
275
275
3307
3332
318
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Matches 6
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                         Ocellar Opsin.
Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
NCBI_TaxID=6850;
                                                                                                        7 (POTENTIAL).
CYTOPLASMIC.
BY SIMILARITY.
RETINAL CHROMOPHORE (BY SIMILARITY).
                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                           .,
                                                                                                                                                                          Score 43; DB 1; Length 376; Pred. No. 21;
                                                                                                                                                                                           Indels
                                                                                                                                                  LINKED (GLCNAC. . .) (PC CCE401766AB06F26 CRC64;
                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                        3 (POTENTIAL). CYTOPLASMIC.
                                                                EXTRACELLULAR.
5 (POTENTIAL).
                                                                                        6 (POTENTIAL).
EXTRACELLULAR.
                                                                                                                                                                                           3; Mismatches
                                                         4 (POTENTIAL)
                        2 (POTENTIAL)
                CYTOPLASMIC
                                                                                 CYTOPLASMIC
                                                                                                                                                           42139 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L03792; AAA28274.1; -. EMBL; L03782; AAA02499.1; -. PIR; A48197; A48197. HSSP; P02699; 1EDV.
                                                                                                                                                                          39.8%;
                                                                                                                                                                                                          PDINPAWYASRGI 14
                                                                                                                                                                                                                          40 PPMNPLWYSILGV 52
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                 193
376 AA;
                                                                                                                                                                          Query Match
Best Local Similarity
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P35361;
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DOMAIN
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CARBOHYD
CARBOHYD
                                                                                                         FRANSMEM
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                                                                                                                                                                                          Matches
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InterPro; IPR001276; GPCR_Rhodpsn.
InterPro; IPR00176; Opsin.
PETAL; PR001277; GPCRHODOPSN.
PROSTIE; PS00237; GPCRHODOPSN.
PROSTIE; PS00237; GPROTEIN RECEP_F1_1; 1.
PROSTIE; PS00238; OPSIN; 1.
PROSTIE; PS00238; OPSIN; 1.
PROSTIE; PS00238; OPSIN; 1.
Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision; DOMAIN

1 46 EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE-22608306; PubMed-12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura A., "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
1.4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching enzyme) (BE) (1,4-alpha-D-glucan:1,4-alpha-D-glucas).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 (POTENTIAL).
EXTRACELULAR.
5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC.
EXTRACELULAR.
7 (POTENTIAL).
CYTOPLASMIC.
BY SIMILARITY.
RETINAL CHROMOPHORE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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SETALINE-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-21477403; PubMed=11572948;
MEDLINE-21477403; PubMed=11572948;
Omutra S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitiis: deducing the ability of producing secondary
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKED (GLCNAC. . .) (PC FA9647C40531CBF8 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 1;
Pred. No. 21;
3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (POTENTIAL).
CYTOPLASMIC.
2 (POTENTIAL).
EXTRACELLULAR.
3 (POTENTIAL).
CYTOPLASMIC.
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Job time : 5.23256 secs
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                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZU-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase).
ARGC OR BH2900.
                            FUNCTION: Catalyzes the formation of the alpha-1,6-glucosidic
linkages in glycogen by scission of a 1,4-alpha-11,8ked
oligosaccharide from growing alpha-1,4-glucan chains and the
subsequent attachment of the oligosaccharide to the alpha-1,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A. STRAIN=C-125 / JCM 9153; MEDLINE=C-125 / JCM 9153; MEDLINE=20512582; PubMed=11058132; Makamin K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                                                                                                    position (By similarity).
CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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SUBUNIT: Monomer (By similarity).
SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
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TIGRPAMs; TIGR01515; branching enzym; 1.
Glycogen biosynthesis; Transferase; Glycosyltransferase;
Complete proteome.
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP005022; BAC70516.1; -.
HAMAP, MF 00685; 1.1
InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR006407; Alpha amyl cat.
InterPro; IPR006407; Alpha amyl cat.
InterPro; IPR004193; Glybo hydro 13N.
Pfam; PF00128; alpha amylase; 1.
Pfam; PF00128; isoamylase, N; 2.
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Nat. Biotechnol. 21:526-531(2003).
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28-FEB-2003 (Rel. 41, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.8%;
72.7%;
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les 8; Conservative
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638 AA,
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Q9K8V2;
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SEQUENCE
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ARGC_BY
DACGE BY
DT 28-FEB-DT 28-FE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                       5-semialdehyde + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Nucleic Acids Res. 28:4317-4331(2000).
-!- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+)
+ phosphate = N-acetyl-5-glutamyl phosphate + NADPH.
-!- PATHWAY: Arginine biosynthesis; thins step.
-!- PATHWAY: LOCATION: Cytoplasmic (Probable).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the NAGSA dehydrogenase family. Subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BMBL, AP001517; BAB06619.1; -.
PIR; D84012, D84012.
HAMAP, MF_00150; -1.
InterPro; IPR000534; Semialdh_dh.
Pfam; PF01714; Semialdhyde_dh; 1.
Pfam; PF02774; Semialdhyde_dh; 1.
Prom; PF03774; Semialdhyde_dh; 1.
PROSTE; PS01224; ARGC; 1.
PROSTE; PS01224; ARGC; 1.
PROSTE; PS01224; ARGC; 1.
Arginine biosynthesis; Oxidoreductase; NADP; Complete proteome.
ACT SITE 149
BY SIMILARITY.
SEQUENCE 345 AA; 38188 MW; 3E9F45DD09FC68EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 345;
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Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August 12, 2004, 14:44:53
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52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Q92ve3 arabidopsis Q9rji0 streptomyce Q9bj9 neurospora Q9bj9 neurospora Q9ril0 streptomyce Q12rl7 xenopus lae Q8d718 human immun Q93lz7 streptomyce Q7xmh8 oryza sativ Q20170 caenorhabdi Q7455 brachycentr Q8644 homo sapien Q81642 bomo sapien Q81742 homo sapien Q81741 xylella fas Q8776 homo sapien

Q7zv60 brachydanio O27142 methanobact Q91gz0 oryza sativ

ALIGNMENTS

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QBWN12;
QBWN12;
QBWN12;
QBWN12;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Preproprolactin-releasing peptide.
Preproprolactin-releasing peptide.
Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Cutters D.H.L., Barclay J.L., Anderson S.T.; "Unlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T.; "Prolactin-releasing peptide (PrRP) in the ewe: cDNA cloning, mRNA distribution and effects on prolactin secretion in vitro and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 95.4%; Score 103; DB 6; Length 98; Local Similarity 94.7%; Pred. No. 1e-08; les 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vivo.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF450453; AAL47178.1; -.
SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAAB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
QBRO54
QBRU54
QBRU10
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QBRU10
QBRU72
QBUXP2
QBUXP2
QBUXP3
QCXMH8
QCXMH8
QCXMH8
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QC
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Q7ZV60
Q9LGZ0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 12, (TrEMBLrel. 12, 1) (TrEMBLrel. 19, 1)
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  Q9W624;
01-NOV-1999 (
01-NOV-1999 (
01-DEC-2001 (
  744
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Best Local S:
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8wn12 ovis aries
                                                                                           August 12, 2004, 14:37:35 ; Search time 27.5581 Seconds (without alignments) 228.984 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                   1017041
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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1 TPDINPAWYASRGIRPVGRX 20
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sp_virus:*
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sp_unclassified:*
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sp_plant:*
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Gapop 10.0 , Gapext
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sp_bacteria:*
sp_fungi:*
sp_human:*
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length: 2000000000
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Maximum DB
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Kurosawa H., Inukal T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
Rakestraw K.M., Naeve C.W., Look T.A.;
Submitted (AFR-1998) to the EMBL/Genbank/DDBJ databases.
[2]
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                                                  SEQUENCE FROM N.A.
De Haan M., Maarse A.C., Grivell L.A., Mewes H.W., Lemcke K.,
Mayor K.F.X., Quetior F., Salancubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 10; Length 790;
Pred. No. 9.6;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 4; Length 54;
Pred. No. 1.1;
1; Mismatches 7; Indels
                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132959; CAB71097.1; -.
PIRP, T47959; T47959.
Hypothetical protein.
SEQUENCE 790 AA; 87376 MW; B222724B75690F30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawlor S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035608; CAB55682.1;
NON TER 54 54 54 54 54 54 54 670 670 877 861 89 F CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Sushi-repeat protein (Sushi-repeat containing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0cr-2003 (TrEMBLrel. 25, Created)
01-0cr-2003 (TrEMBLrel. 25, Last sequence update)
01-0cr-2003 (TrEMBLrel. 25, Last annotation update)
01-0cr-2003 (TreMBLrel. 25, Last annotation update)
D4749477.3 (Sushi-repeat protein (SRFUL)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PDINPAWYASRGIRPVGR 19
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Best Local Similarity 55.6%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.28;
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nes 8; Conserv
                                                                                                                                                                                       SEQUENCE FROM N.A.
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NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                         Carassius auratus (Goldfish).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicoryledoms; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schleener H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula strain 1.";
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Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                  / Match 72.2%; Score 78; DB 13; Length 11
Local Similarity 57.9%; Pred. No. 0.00012;
les 11; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
EMBL; BX224145; CAD75095-1; -
Hypothetical protein; Complete proteome.
SEQUENCE 1120 AA, 123221 MW; 67C757B73421BF9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                TISSUE=Brain;
Satake H., Minakata H., Fujimoto M.;
Satake H., Minakata H., Fujimoto M.;
Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 FW; D5DC4CB22038C2B0 CRC64;
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Last annotation update)
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202 EISPAWWAKMGIRP 215
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RB6951.
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Matches 9, Conserv
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                                                                                                                                                                                          SEQUENCE FROM N.A.
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Q9M371;
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Q9M371
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Pfam; PF00109; ketoacyl-synt; 1.
Pfam; PF02801; ketoacyl-synt C; 1.
Pfam; PF00550; pc-binding; 2.
Pfam; PF00555; Thioesterase; 1.
                                                                                                                                                                                                                                             EMBL; AE004642; AAG05539.1; -.
                Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 TPDINP-WFLORSGRP 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYASRGIRP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 62.59
Hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                              opportunistic pathogen."
Nature 406:959-964(2000)
                              NCBI_TaxID=287;
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ID Q8FM04
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              Huang C.-H., Chen H., Peng J., Chen Y., "Cloning and characterization of the sushi-repeat containing protein (SRP) as a novel interaction partner of Rh type C glycoprotein
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                       (RhCG) "; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF060567; AAC17665.1. -
EMBL; AF060567; AAC17665.1. -
EMBL; AF060567; AAC17665.1. -
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR001410; Hyalin.
InterPro; IPR000440; Sushi_SCR_CCP.
Pfam; PF02494; HYR; 1.
Pfam; PF02494; HYR; 1.
Pfam; PF026064; Sushi_3: 3.
PROSITE; PS000686; CYTOCHROWE P450; 1.
SEQUENCE 465 AA; 52971 NW; 4D752B187FF3EFB8 CRC64;
                                                                                                                                                                                                                                                          Query Match
47.2%; Score 51; DB 4; Length 465;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.2%; Score 51; DB 4; Length 465; 50.0%; Pred. No. 11; ive 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC020733; AH207733.1; -
GO00006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR003410; Hyalin.
InterPro; IPR003416; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00032; CCP; 3.
PROSITE; PS00086; CYTOCHROME_P450; 1.
SEQUENCE 465 AA; 52957 MW; 3D7229487DA1B8BD CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PA2151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.v.
Best Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissum=Placenta;
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Q8WW85
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TRAIN-YS-314 / AJ 12110 / DSM 44549 / JCM 11189;

STRAIN-YS-314 / AJ 12110 / DSM 44549 / JCM 11189;

A Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,

A Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

A Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

A Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

A Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

A Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,

A Ikeo M., Suzuki M., Nishio M., Nishio Y.,

Sumited (MAY-2002) E., Policy J., Corpus G., Collofors, P., Piderson C., Pickolofors, P., Piderson C., Pickolofors, P., Piderson C., Pickolofors, P., Retoacyl L., Suzuki M., Carans.

B InterPro; IPRO01227; Activati G., Polick M., R., Milloster M., R., Milloster M., R., Milloster M., 
SEQUENCE FROM N.A.
STRAINS-ATC 15692
STRAINS-ATC 15692
STRAINS-ATC 15692
STRAINS-ATC 15692
STOVER C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.C., Brinkman F.S.L., Hufnagle W.O., Kowallik D.J., Lagrow M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Tall_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR, F83376; F83376.

GO, GO:0003779; F:actin binding; IEA.

GO, GO:0004556; F:alpha-amylase activity; IEA.

GO, GO:0005975; F:carbohydrate metabolism; IEA.

InterPro; IPR001589; Actbind actini.

InterPro; IPR001589; Actbind actini.

InterPro; IPR001697; Alpha_amylact.

PROSITE; PS00019; ACTININ 1; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 664 AA; 76329 MW; 8FS9FEED54C308AD CRC64;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative polyketide synthase.
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Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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Best Local Similarity
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01-JUN-1998
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                                          SEQUENCE
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRLL 8165;
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRLL 8165;
STRAIN=21477403; PubMed=11579248;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
                                                                                                      DB 16; Length 1654;
65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.4%; Score 49; DB 16; Length 187; 55.6%; Pred. No. 8.6;
                                                                                                                                              5; Indels
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                                                              1654 AA; 176466 MW; BBB60E7E3CE55CBB CRC64;
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EMBL; BX294142; CAD7414.1.; -.

Hypothetical protein; Complete proteome.

SEQUENCE. 187 AA; 20737 MW; AFF81D5104D7AF21 CRC64;
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Last annotation update)
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                      187 AA
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                                                                                                                                              2; Mismatches
PROSITE; PS50075; ACP_DOMAIN; 3.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
                                                                                                      Score 50;
Pred. No.
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                                                                                                   Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
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                                          Complete proteome.
SEQUENCE 1654 AA
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Q821E7;
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Q7URC6
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0821E7
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AC 0821E
DT 01-07
DT 01-07
DF 01-07
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OS STREA
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H., "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                 "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";

Nat. Biotechnol. 21:256-531 (2003).

ENBL, ADO05034; DAC70922.1; -

GO; GO:0009318; C:exodeoxyribonuclease VII complex; IEA.

GO; GO:0008855; F:exodeoxyribonuclease VII activity; IEA.

GO; GO:0000865; F:exodeoxyribonuclease VII activity; IEA.

GO; GO:0000876; F:nucleic acid binding; IEA.

Interpro; IPR00475; Exonuc_VII_L.

Interpro; IPR00475; Exonuc_VII_L.

Pfam; PF02601; Exonuc_VII_L; 1.

Pfam; PF02601; Exonuc_VII_L; 1.

Pfam; PF01336; TRNA_anti; 1.
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                                                                    M., Kikuchi H., Shiba
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GO; GO: 0005215; F: catalytic activity; IEA.
GO; GO: 0005215; F: transport activity; IEA.
GO; GO: 0006810; P: transport; IEA.
InterPro: IPR001330; Prenyltrans.
InterPro: IPR008930; Parp Cransporter.
InterPro: IPR008930; Tarp cyc_toroid.
Pfam; PF00432; prenyltrans; 2.
PROSITE; PS00216; SUGAR_TRANSPORT 1; 1.
Hypothetical protein; Ocmplete profesome.
SEQUENCE 284 AA; 32319 MW; REDETBC3711D3815 CRC64;
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165; MEDLINE=22608306; PubMed=12692562;
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(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                        Ikeda H., Ishikawa J., Hanamoto A., Shinose
Sakaki Y., Hattori M., Omura S.;
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PH1420.
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43.5%; Score 47; DB 17; Length 284;

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Conservative
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Best Local Similarity
8; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2371;
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MEDLINE=22421331; PubMed=12533478;
Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
Van Sluys M.A., de Oliveira M.C., Machado L.E.A., da Silva A.C.R., Moon D.H.,
Miyaki C.Y., Furlan L.R., Camargo L.E.A., Ferro M.I.T., da Silva F.R.,
Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae, Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-TUN-2003 (TrEMBLrel. 24, Created)
01-TUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCTT-2003 (TrEMBLrel. 25, Last annotation update)
Hydroxybenzoate octaprenyltransferase.
UBIA OR PD0046.
Xylella fastidiosa (strain Temeculal / ATCC 700964).
Anthomonadaceae; Xylella.
Anthomonadaceae; Xylella.
                               ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

"The complete sequence of the Pyrococcus furiosus genome.";

"The complete sequence of the Pyrococcus furiosus genome.";

"The complete sequence of the Pyrococcus furiosus genome.";

"Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

RMEL, ABO10244; AA.81542.1; ---

"GO; GO:0003824; F:Caralytic activity; IEA.

"GO; GO:0003824; F:Caralytic activity; IEA.

"GO; GO:0005215; F:Cransporter activity; IEA.

"GO; GO:0005216; F:Cransporter activity; IEA.

"InterPro; IPR001330; Prenyltrans.

InterPro; IPR00830; Prenyltrans.

"Rema; PF00432; prenyltrans; 2.

"PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome.
SEQUENCE 284 AA; 32302 MW; 1D4C5746A1831390 CRC64;
                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein PF1418.
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                                                                                                                                                                                                                                                                              284 AA.
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  d. No. 28;
Mismatches
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  Pred. No.
                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                     217 PYIEPTFYALRGLELLGR 234
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|PYIEPTFYALRGLELLGR 234
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ص
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50.0%;
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50.0%;
                                                                                 2 PDINPAWYASRGIRPVGR
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Best Local Similarity 50.v.
Best Local 9; Conservative
                               Conservative
                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus furiosus.
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                        Q8U112;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q87F82;
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                                                                                                                                                                                                                                                                           Q8U112
                               Matches
                                                                                                                                                                                                                      RESULT 13
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STRAINE=20365717; PubMed=10910347;

STRAINE=20365717; PubMed=10910347;

RA Alvarenga R., Alves L.M.C., Arraya J.E., Babia G.S., Baptista C.S.,

Barross M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,

Barross M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,

RA Benen M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,

RA Clauto N.B., Colombo C., Costa R.F., Costa M.C.R., Costa-Neto C.M.,

RA Farga J.S., Franco M.C., Franco M.C., Frome M., Purlan L.R.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Genes S.L., Gruber A.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Genes S.L., Gruber A.,

RA Garnier M., Goldman B.E., Langrete F., Lambais M.R., Leite L.C.C.,

RA Marques M.V., Martins E.M.L., Martins E.M.F., Martinka A.Y.,

RA Mardues M.V., Martins E.A.L., Martins E.M.F., Martinka A.Y.,

RA Mardues M.V., Nartins E.A.L., Martins E.M.F., Martinka A.Y.,

RA Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

RA Gollveira M.C., de Oliveira R.C., Pereira H.A. Jr., Pesquero J.B.,

RA Goldwar G.A.G., Pereira H.A. Jr., Pesquero J.B.,

RA Goldwar G.A.G., Santelli R.V., Sawasaki H.E.,

RA G. Silva A.C.R., Salva E.M., da Silva M.A. Jr.,

RA da Silva A.C.R., Salva E.M., da Silva M.A., Tasi S.M., Tsuhako M.H.,

RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;

RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;

RA Lade Genous E.G. Hardenson M.S., Tsuhako M.H.,

RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;

RA BEL, Abcolse G. the plant pathogen Xylella fastidiosa.";

RH BMEL, ABCO13860, AAFG2881.1; --
da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T., Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D., de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G., Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                       sequences of Pierce's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                   "Comparative analyses of the complete genome sequences of P disease and citrus variegated chlorosis strains of Kylella fastidiosa.";
J. Bacteriol. 185:1018-1026(2003).
GO: 00102553; AAO27953.1;
GO: 00.0016020; C:membrane; IEB.
GO: GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000537; UblA.
Pfam; PF01040; UblA; 1.
PROSITE; PS00943; UBLA; 1.
Transferae; Complete proteome.
SEQUENCE 299 AA; 33965 NW; CE8C74395056D8F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hydroxybenzoate octaprenyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.5%; Score 47; DB 16;
53.3%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDPYWKLARGDRPVG 34
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Search completed: August 12, 2004, 14:49:06 Job time : 30.5581 secs

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August 12, 2004, 14:37:35 ; Search time 42.4419 Seconds (without alignments) 133.146 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                            1586107
5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                        1586107 segs, 282547505 residues
GenCore version
Copyright (c) 1993 - 2004
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                          108
1 TPDINPAWYASRGIRPVGRX 20
                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                      US-09-700-643A-5
                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqq1980s;*
geneseqq1990s;*
geneseqq2000s;*
geneseqq2001s;* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* 1: geneseqp1980s:* geneseqp2003as:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

# Res

ы	Aaw31394 Human typ	Aaw97236 Human typ	Aay49294 19P2 liga	ŧ٥	Aab90992 Prolactin	Aag62534 Human CRH	Aae26404 Human PrR	Abu60846 Peptide p	Aaw31395 Human typ	Aab10366 Human oxy	Aag62535 Human CRH	Abu60847 Peptide p	6	Aab10367 Human oxy	Aag62536 Human CRH	Abu60848 Peptide p	Aay49299 19P2 liga	Aaw31391 Human typ	Aaw87615 Human 19P	Aaw97235 Human typ	Aay49291 19P2 liga	Aab10362 Human oxy	Aab90991 Prolactin	Aab90995 Prolactin	Aag62531 Human CRH
ID	AAW31394	AAW97236	AAY49294	AAB10365	AAB90992	AAG62534	AAE26404	ABU60846	AAW31395	AAB10366	AAG62535	ABU60847	AAW31396	AAB10367	AAG62536	ABU60848	AAY49299	AAW31391	AAW87615	AAW97235	AAY49291	AAB10362	AAB90991	AAB90995	AAG62531
DB	2	7	m	m	4	4	ഗ	ω	7	ო	4	ø	7	m	4	ø	m	7	7	N	m	m	4	4	4
Length	20	20	20	20	20	20	20	20	21	21	21	21	22	22	22	22	30	31	31	31	31	31	31	31	31
Query Match	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	9.	99.1	99.1	1.66	99.1	99.1	99.1
Score	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107	107
sault No.		7	m	4	'n	9	7	80	0	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25

Human Peptid	AGC/1228 Human pep Aaw31392 Human typ Aab10363 Human oxy AaG6532 Human CRH	Peptid Human Human	Human Peptid		Aaw11370 Bovine G Aaw95185 Bovine pi Abu60830 Peptide p Aaw31374 Bovine G
AAE26401 ABU60843 ABU60827	ADC71228 AAW31392 AAB10363 AAG5532	ABU60844 AAW31393	AAB1U364 AAG62533 ABU60845	AAM912390 AAW97226 AAB10361 AAG62530	AAW31370 AAW95185 ABU60830 AAW31374
444		0 00 0	1 m m r		20 20 20 20 20 20 20 20 20 20 20 20 20 2
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107	107 107 107	107	107	107	103 103 103
222	8 0 H 6	1 6 6 6 1	, w w u	2 W 4 4 2 W O H	4 4 4 4 0 6 4 6

## ALIGNMENTS

This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent. Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland. Fukusumi S; Human type G protein-coupled receptor ligand fragment 4. ď Fujii Habata Y, Kawamata Y, Hosoya M, AAW31394 standard; peptide; 20 AA. Claim 2; Page 185; 258pp; English. 95JP-00343371. 96JP-00059419. 96JP-00211805. 96JP-00246573. 96WO-JP003821. (TAKE ) TAKEDA CHEM IND LTD. (first entry) WFI; 1997-363672/33. N-PSDB; AAV02431. Homo sapiens. WO9724436-A2. 26-DEC-1996; 28-DEC-1995; 15-MAR-1996; 12-AUG-1996; 18-SEP-1996; 06-APR-1998 10-JUL-1997 Hinuma S, Kitada C; AAW31394; RESULT 1 AAW31394 

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disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholactinnemia, diabetes, hypercholactinnemia, diabetes, cancer, pancetitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocereballar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat type ligand; modulation; prolactin secretion; of protein-coupled receptor; GFGR; hypocovarianism; genecyst cacegenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infartility; impotence; amenorthea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Porbes-Albright syndrome; Sheehan syndrome; dyscospermia; contraceptive; placental function; choriocarcinoma; hydaild mole; irruption mole; abortion; unthifity fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
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Pred. No. 1.2e-10;
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100.0%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW97236 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 166; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPDINPAWYASRGIRPVGR 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 AA;
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AAW97236
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Gaps

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brain tumour, emmeniopathy, autoimmune disease, prolattinoma, brain tumour, emmeniopathy, autoimmune disease, prolattinoma, infertility, impotence, amenorthes, galactorrhea, acromegaly, Chiari-Frommel Syndrome, Argonz-del Castilo syndrome, Porbes Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful in diagnosis, as drugs and in studying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody, 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic.
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                                                                                                                                                                                                       Length 20;
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                                                                                                                                                                                                      Score 107; DB 2; Pred. No. 1.2e-10;
                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New monoclonal antibodies, useful in di
diseases related to ligand abnormality.
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                                                                                                                                                                                         99.1%; Sc._
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19P2 ligand peptide fragment
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                                                                                                                                                                                                                                       19; Conservative
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                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                        Sequence 20 AA;
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Length 20;

99.1%; Score 107; DB 3; 1 100.0%; Pred. No. 1.2e-10;

Query Match Best Local Similarity

The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing promoting prolactin secretion can be used for treating or preventing hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin

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us-Uy-/UU-643a-5.rag

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Sequence 20 AA;
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10-SEP-1999;
15-OCT-1999;
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                                                                               Synthetic.
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                                                                                                                                                                      Human, oxytocin secretion promoter, G protein-coupled receptor protein, treatment, disease, pain, atonic bleeding, uterine recovery failure, cow; caesarean section, artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                          Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
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Gaps
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                                                                                                                                                     Human oxytocin secretion promoting peptide SEQ ID NO: 35.
 Indels
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0
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                  Hinuma S;
                                                                                          AAB10365 standard; peptide; 20 AA.
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                                 1 TPDINPAWYASRGIRPVGR 19
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Best Local Similarity 100.0
These 19; Conservative
                                                                                                                                  24-NOV-2000 (first entry)
 19; Conservative
                                                                                                                                                                                                                                                                                                                                                    Matsumoto H, Kitada C,
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-452298/39.
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AAB10365
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a caactive group (III) etg. succinimidyl and mademido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a competitive set therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth components and neurotransmitters, to protect them from peptidas activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent competides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Companies the action of peptidases to increase length of activity (half contracts the action of peptidases to increase length of activity (half intracellular uptake and interference with physiological processes. AAB30829 to AAB3241 represent public and be used in the companies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
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                                                                         Protection, endogenous therapeutic peptide; peptidase; conjugation; blood component, modification; succinimidy1; maleimido group; amino; hydroxy1; thio1; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ezrin AM, Milner PG, Holmes DL,
Prolactin releasing peptide SEQ ID NO:166
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99US-0153406P.
99US-0159783P.
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Best Local Similarity 100.
Matches 19; Conservative
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The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PrRP) receptor (GPRIO) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. PrRP receptor agonists may be used to treat common disorders which lead psychogenic hypersomnia. PrRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep disorder and psychologic insomnia. The present sequence is human PrRP-31 C-terminal peptide, PrRP-20
                                                                                  Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide production by gene recombination associated peptide #30.
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Pred. No. 1.2e-10;
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                                                                                                                                                                                          Disclosure; Page 25; 35pp; English.
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100.0%; Pred
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Matches 19; Conservative
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                                            WPI; 2002-403931/43
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Civelli O,
                                                                                                                                                  antagonist
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                                                                                                                                                                                                                                                                                                                                                                              Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; wakefulness; sleep disorder; prolactin releasing peptide receptor; Prep; GRR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea; insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure; anticonvulsant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for tracting, preventing or ameliorating diseases associated with CRH secretion such as hyperconism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nauses, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                              Matsumoto H, Hinuma S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE26404 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 75; 90pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPDINPAWYASRGIRPVGR 19
                                                                                                                                                17-NOV-2000; 2000WO-JP008119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-AUG-2001; 2001US-00932161.
                                                                                                                                                                                        18-NOV-1999; 99JP-00327900
26-SEP-2000; 2000JP-00297073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-2000; 2000US-00560915.
                                                                                                                                                                                                                                                    (TAKE ) TAKEDA CHEM IND LTD.
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                                                                                                                                                                                                                                                                                                                                   WPI; 2001-355552/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002037533-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 AA;
                                                           WO200135984-A1
                      Homo sapiens.
                                                                                                                                                                                     18-NOV-1999;
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                                                                                                        25-MAY-2001.
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                                                                                                                                                                                                                                                                                              Kitada C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
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Matches
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Gaps

transient brain ischaemia, epilepsy

spinal injury,

rheumatoid arthritis,

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excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GRRB ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor; ligand binding; pharmaceutical; modulator;
pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide for G protein-coupled receptor - acts by modulating
on in the central nervous system, pancreas and pituitary gland.
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                                                                                                                                                                                                             Length 20,
                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G protein-coupled receptor ligand fragment 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hosoya M, Fujii
                                                                                                                                                                                                               Score 107; DB 6; I
Pred. No. 1.2e-10;
                                                                                                                                                                                                             Query Match
99.1%; Score 107; DE
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 19; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 186; 258pp; English.
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96JP-00059419.
96JP-00211805.
96JP-00246573.
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                                                                                                                                                                                                                                                                                                                                                                                                          AAW31395 standard; peptide;
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                                                                                                                                                                             Sequence 20 AA;
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15-MAR-1996;
12-AUG-1996;
18-SEP-1996;
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        amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, steporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. wes pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Human oxytocin secretion promoting peptide SEQ ID NO:
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Local Similarity 100.0%; Pred. No. 1.2e-10;
1es 19; Conservative 0; Mismatches 0;
                                                                                                                                             Query Match
99.1%; Score 107; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 19; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 63;
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                                                                                                                   Sequence 21 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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for dise
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AAB10366
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95JP-00343371.
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96JP-00246573.
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                                                                                                                                                                                                    Suenaga M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                              WPI; 2003-129302/12.
     gene recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21 AA;
                                                            WO200292829-A1
                                Homo sapiens
                                                                                                                                                                                                  Nishimura O,
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12-AUG-1996;
18-SEP-1996;
                                                                                      21-NOV-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of G protein receptor ligand or peptide for controlling corticotropin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nauses, pigmentation, hypoagnadism, hair loss, and hypotension), adread gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                 Human, corticotrophin releasing hormone, CRH, G protein receptor ligand, analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease, adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence describes a method of controlling the secretion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107; DB 4; Length 21;
Pred. No. 1.2e-10;
0; Mismatches 0; Indels
                                                                                                                                                                      Human CRH releasing protein related peptide SEQ ID NO: 36.
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Kitada C, Matsumoto H, Hinuma
                                                                                    AAG62535 standard; peptide; 21
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Local Similarity 100.0%; Pres 19; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             releasing hormone secretion.
                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                  WO200135984-A1
                                                                                                                                                                                                                                                                                                                                                                    18-NOV-1999;
                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                        24-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match.
                                                                                                                AAG62535;
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                                                         RESULT 11
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ID ABU6
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AC ABU6
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DT 06-N
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DE PEPT
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KW PEPT
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The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a texaget peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptides and GRRB ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                            Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
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pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human type G protein-coupled receptor ligand fragment 6.
                                                                                                                                                                                                                                                         Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 69; 87pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW31396 standard; peptide; 22 AA
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.6-MAY-2002; 2002WO-JP004735.
                                                                                      17-MAY-2001; 2001JP-00147341
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in AAW31390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prohylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, cultrophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, panoreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinal pinary, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinal pinary, transient brain ischaemia, epilepsy, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                               Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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                        Fukusumi
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                                                                                                                                                                                                                                                                                                                                                                                                                                   99.1%; Score 107; DB 2; Length 22; 100.0%; Pred. No. 1.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human oxytocin secretion promoting peptide SEQ ID NO: 37.
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                        n,
                      Fujii
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                        Hosoya M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.3 Mismatches
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                        Kawamata Y,
                                                                                                                                       Claim 2; Page 186; 258pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pr
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPDINPAWYASRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPDINPAWYASRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB10367 standard; peptide; 22
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(TAKE ) TAKEDA CHEM IND LID.
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                        Habata Y,
                                                            WPI; 1997-363672/33.
N-PSDB; AAV02433.
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                        Hinuma Kitada (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor Thisand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hyperotrisolaemia, secondary or chronic hypoatencocriticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                               This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. wea pains and atonic bleeding, before and after expulsion of placenta, uterina recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                              drugs
Physiologically-active polypeptide recognized as ligand by G protein-
coupled receptor protein, for promoting secretion of oxytocin, as drugs
for diseases relating to oxytocin secretion and in veterinary medicine.
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                                                                                                                                                         Disclosure; Page 64; 72pp; Japanese.
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26-SEP-2000; 2000JP-00297073.
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Best Local Similarity
Matches 19; Conserv
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Search completed: August 12, 2004, 14:43:55 Job time: 42.5669 secs

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Sequence 17, Appl
Sequence 6, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 197, Appl
Sequence 187, Appl
Sequence 169, Appl
Sequence 169, Appl
Sequence 169, Appl
Sequence 169, Appl
Sequence 26, Appl
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Sequence 268092,
Sequence 30, Appl
Sequence 4642, Ap
                                                                                          Sequence 84, 7
Sequence 86, 7
Sequence 88, 7
Sequence 17, Ap.
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Sequence 17, A
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; Batent No. US20020037533A1
; GENERAL INFORMATION:
    APPLICANT: Civelli, Olivier
; APPLICANT: Civelli, Olivier
; TITLE OF INVENTION: Screening and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep
; TITLE OF INVENTION: Promoting Wakefulness and Sleep
; FILE REPERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastsEQ for Windows Version 4.0
; SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
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3 US-10-044-592-41
3 US-10-044-592-38
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3 US-10-044-592-84
3 US-10-044-592-86
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4 US-10-044-592-86
4 US-10-044-592-86
5 US-10-044-592-86
5 US-10-044-592-96
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7 US-10-044-593-133044
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Pred. No. 2e-09;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/10096777; Publication No. US20030171270A1; GENERAL INFORMATION: APPLICANT: Civelli, Olivier APPLICANT: Lin, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th 99.1%; Scc
| Similarity 100.0%; Pr
| 19; Conservative 0;
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; ORGANISM: Homo Sapien
US-09-932-161-18
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Sequence 15, Appl
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Sequence 18, Appl
                                                                                                                                              August 12, 2004, 14:49:10 ; Search time 35.3488 Seconds (without alignments) 177.617 Million cell updates/sec
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Sequence 13, A
Sequence 39,
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| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-044-592-43

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Listing first 45 summaries
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108
1 TPDINPAWYASRGIRPVGRX 20
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Match
                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                        Scoring table:
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1007
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                                                                                                        OM protein
                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                     Run on:
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No.
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95.4%; Score 103;
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; Sequence 92, Application US/10044592
; Publication No. US20020143152A1
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27, Application US/10044592 Publication No. US20020143152A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                        12 TPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                   1 TPDINPAWYASRGIRPVGR 19
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                                                                                                                                                  19; Conservative
  ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-096-777-15
                                                                                                   Query Match
Best Local Similarity
Matches 19; Conserv
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US-10-044-592-27
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PUBLICATION
GENERAL INFORMATION:
GENERAL INFORMATION:
JAPPLICANT: Lin, Steven
JILLE OF INVENTION: Relations and Methods
JILLE OF INVENTION: Relation To Prolactin Releasing Peptide (PTRP)
JILLE OF INVENTION: Therapeutic Compositions and Methods
JILLE OF INVENTION: Relation TO Prolactin Releasing Peptide (PTRP)
JILLE OF INVENTION: P-UC 3534
CURRENT FILING DATE: 2002-03-12
FILOR PEPTICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
JOSOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 31
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating TO Prolactin Releasing Peptide (PRRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR PILILGATION NUMBER: US/09/560,915
PRIOR PILILGATION NUMBER: US/09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 20
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GENERAL INFORMATION:
GENERAL INFORMATION:
TATLE OF INVENTION: Steven
TITLE OF INVENTION: Promoting and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.1%; Score 107; DB 14; Length 20; Best Local Similarity 100.0%; Pred. No. 2e-09; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.1%; Score 107; DB 9; Length 31; 100.0%; Pred. No. 3.1e-09; tive 0; Mismatches 0; Indels
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ORGANISM: Homo Sapien
US-09-932-161-15
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ORGANISM: Homo Sapien
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US-10-096-777-15
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US-09-932-161-15
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APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Pukusumi, Shoji
ITILE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 24631052P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-00
PRIOR APPLICATION NUMBER: US 09/4039
PRIOR FILING DATE: 1998-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: UP 9-109974
PRIOR FILING DATE: 1998-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SOFTWARE:
SEQ ID NO 92
LENGTH: 87
TYPE: PRT
CORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Rikmani, Shoji
TITLE OF INVENTION: POLYPeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: UP 9-109974
PRIOR FILING DATE: 1996-04-27
PRIOR FILING DATE: 1996-04-27
PRIOR FILING DATE: 1996-04-27
SPRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 27
LENGTH: 19
     Length 31;
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99.1%; Score 107; DB 14;
100.0%; Pred. No. 3.1e-09;
ive 0; Mismatches 0;
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99.1%; Score 107; DB 13;
Best Local Similarity 100.0%; Pred. No. 8.7e-09;
Matches 19; Conservative 0; Mismatches 0;
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Sequence 16, Application US/10096777

Publication No. US20030171270A1

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

APPLICANT: Lin, Steven

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)

TITLE OF INVENTION: Relating TO Prolactin Releasing Peptide (PrRP)

TITLE OF INVENTION: Relating TO Prolactin Releasing Peptide (PrRP)

FILE REFERENCE: D-0.3534

CURRENT FILING DATE: 2002-03-12

PRIOR FPLING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PRASEQ for Windows Version 4.0

LENGTH: 20
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APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
IIILE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463U32P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: 08 09/403639
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: UP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 43
LENGTH: 21
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Pred. No. 8.7e-09;
0; Mismatches 1; Indels
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Sequence 44, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

APPLICANT: Fukusumi, Shoji

TITLE OF INVENTION: Polypeptides, their Production and Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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8.3e-09;
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Best Local Similarity 94.7%; Pred. No. 8
Matches 18; Conservative 0; Mismatch
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Best Local Similarity 94.7%;
Matches 18; Conservative 0
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CORGANISM: Bos taurus
US-10-096-777-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Bovine US-10-044-592-43
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US-10-044-592-43
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Sequence 42, Application US/10044592

Sequence 42, Application US/10044592

Publication No. USSO020143152A1

GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 2002-01-10
PRIOR PILING DATE: 1999-25-10
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE:
SEQ ID NO 42

LENGTH: 20
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Pred. No. 8.3e-09;
0; Mismatches 1; Indels
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95.4%; Score 103; DB 9; Length 20;
Best Local Similarity 94.7%; Pred. No. 8.3e-09;
Matches 18; Conservative 0; Mismatches 1; Indels
                          Indels
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lin, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REPERENCE: P-UC 4679
CURRENT PLINGE DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US/09/932,161
PRIOR APPLICATION NUMBER: US/09/915
PRIOR FILING DATE: 2000-04-28
Best Local Similarity 94.7%; Pred. No. 7.9e-09;
Matches 18; Conservative 0; Mismatches 1;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 20
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bos taurus
US-09-932-161-16
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APPLICANT: Lin, Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
FILE REPERENCE: P-UC 5334
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2006-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 31
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1S-10-04-15-52-40

Sequence 40, Application US/10044592

Publication No. US20020143152A1

GENERAL INPORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: HOANSUMI, Shoji
ITILE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463032p
FURRENT FILING DATE: 2002-01-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-10
PRIOR FILING DATE: 1998-04-10
PRIOR FILING DATE: 1998-04-10
PRIOR FILING DATE: 1998-04-10
SEQ ID NOS: 96

SEQ ID NOS: 96

LEMENT OF APPLICANT OF APPLICA
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95.4%; Score 103; DB 14; Length 31;

Best Local Similarity 94.7%; Pred. No. 1.3e-08;

Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                          Length 31;
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Pred. No. 1.3e-08;
0; Mismatches 1;
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ilarity 94.7%;
Conservative (
PRIOR FILING DATE: 1997;
NUMBER OF SEQ ID NOS: 5;
SOFTWARE:
SEQ ID NO 39
LENGTH: 31
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Best Local Similarity
Matches 18; Conserva
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CRGANISM: Bos taurus

US-10-096-777-13
                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-39
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; Sequence 39, Application US/10044592
; Publication No. US202020143152A1
; GENERAL INFORMATION:
    APPLICANT: Hinuma, Shuji
; APPLICANT: Hinuma, Shuji
; TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
; CURRENT APPLICATION NUMBER: US/10/044,592
; CURRENT PILING DATE: 2002-01-10
; PRIOR FILING DATE: 1999-25-10
; PRIOR FILING DATE: 1998-04-27
; PRIOR FILING DATE: 1998-04-27
; FRIOR PILING DATE: 1998-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/09932161
Patent No. US20020037533A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 103; DB 13; Length 22;
Pred. No. 9.2e-09;
0; Mismatches 1; Indels
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                          CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR PPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/UP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1997-04-28
SOFTWARE: SOFTWARE: 1997-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPDINPAWYASRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TPDINPAWYAGRGIRPVGR 19
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Best Local Similarity 94.7%;
Matches 18; Conservative (
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Matches 18; Conservative
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CRGANISM: Bos taurus
US-09-932-161-13
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Bovine
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US-09-932-161-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-044-592-44
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Gaps

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us-09-700-643a-5.rapb
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Query Match 95.4%; Score 103; DB 13; Length 32; Best Local Similarity 94.7%; Pred. No. 1.3e-08; Matches 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                Search completed: August 12, 2004, 15:22:51
Job time : 35.3488 secs
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Query Match
99.1%; Score 107; DB 3; Length 20
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels
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MOLECULE TYPE: peptide

US-09-105-678A-46
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46, Appl
Sequence 18, Appl
Sequence 65, Appl
Sequence 67, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 61, Appl
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Appl
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Sequence 64, Appl
Sequence 46, Appl
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                                                             August 12, 2004, 14:37:36; Search time 11.3953 Seconds (without alignments) 90.609 Million cell updates/sec
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Sequence 59, A
Sequence 135,
Sequence 138,
Sequence 30, A
Sequence 4, Ap
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Sequence 6
Sequence 4
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Sequence 6
Sequence 4
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2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-421-208-46
US-09-421-208-46
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US-09-421-208-47
US-09-421-208-47
US-09-421-208-48
US-09-408-476-971-62
US-09-421-208-48
US-08-776-971-138
US-08-776-971-138
US-08-776-971-138
US-08-776-971-138
US-08-776-971-138
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                                                                                                                                                                     389414 segs, 51625971 residues
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                                                                                                                                                                                                                                                       Listing first 45 summaries
                                              OM protein - protein search, using sw model
                                                                                                   US-09-700-643A-5
108
1 TPDINPAWYASRGIRPVGRX 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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                                                                                                                       Sequence:
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34, Appli
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98, 3
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Sequence 46, Application US/09105678A
Fatent No. 61038D4
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SERVINGE.

CORRESPONDED ADDRESS:
ADDRESSEB:
ADDRESSEB:
ADDRESSEB:
ADDRESSEB:
ADDRESSEB:
ADDRESSEB:
ADDRESSEB:
ADDREST:
130 Water Street
CITY:
BOSTON
STATE:
MA
COUNTRY:
USA
ZIP:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER:
PROPOSING SYSTEM:
COMPUTER:
PROPOSING SYSTEM:
COMPUTER:
PRECATING SYSTEM:
COMPUTER:
PRECATING DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
PRINK APPLICATION DATA:
ATORNEY AGENT INFORMATION:
APPLICATION NUMBER:
APPLICATION NUMBER:
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ATORNEY AGENT INFORMATION:
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TELEFHONE:
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US-09-421-208-30

US-09-105-678A-34

US-08-776-971-8

US-09-421-208-34

US-09-60-915-16

US-09-105-678A-35

US-09-105-678A-35

US-09-105-678A-36

US-09-105-678A-36

US-09-105-678A-36

US-09-105-678A-36

US-09-105-678A-36

US-09-115-678A-36

US-09-115-678A-36

US-09-115-678A-36

US-09-115-678A-37

US-09-115-678A-37

US-09-115-678A-37

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US-09-115-678A-37

US-09-115-678A-37

US-09-411-208-37
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Length 20;

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Sequence 46, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 46

. SEQUENCE CHARACTERISTICS:

. LENGTH: 20 anino acids

TYPE: anino acid
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Best Local Similarity 100.
Matches 19; Conservative
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Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: WA
COUNTRY: USA
ZIP: 02109
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compartible
OPERATURS SYSTEM: DOS
SOFTWARE: FASTESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATE:

APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-08-776-971-64
                                                                                                                                            Sequence 64, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
1 TPDINPAWYASRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 20 amino acids
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INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 19; Conserva
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1 TPDINPAWYASRGIRPVGR 19

RESULT 3

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Patent No. 6383764

JARAPLICANT: LIN PORMATION:
APPLICANT: Civelli, Steven
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
CURRENT APPLICATION NUMBER: US/09/560,915
CURRENT FILING DATE: 200-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 20
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APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSED: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                            CITY: Boston
CITY: Boston
CUNTRY: WA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPDINPAWYASRGIRPVGR 19
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ORGANISM: Homo Sapien
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Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                            ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
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Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                          COMPUTER: IBM compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 107; DB 3; 1
Pred. No. 1.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                          PRING DATE: 06-Feb-1997
CLASSIPICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIPICATION: -Unknown>
PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 7/343371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 8/5919
FILING DATE: 18-MAR-1996
APPLICATION NUMBER: UP 8/211805
FILING DATE: 18-MAR-1996
APPLICATION NUMBER: UP 8/246573
FILING DATE: 18-MAR-1996
APPLICATION NUMBER: UP 8/246573
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100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGWENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
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                                                                                                                                                                                                                                                ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
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Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                            STATE: MA
COUNTRY: USA
                                                                                                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-09-421-208-47
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                                          Length 20;
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                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 130 Water Street
STREET: 130 Water Street
STREET: 130 Water Street
STATE: MA
COUNTRY: USA
COUNTRY: USA
MULTER: 02109
MULTER: 02109
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLICATION NUMBER: US/09/105,678A
FILLIG DATE: 26-UUN-1998
                                     Score 107; DB 4; I
Pred. No. 1.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 107; DB 3; 1
Pred. No. 1.3e-10;
                                        Query Match 99.1%; Score 107; DE Best Local Similarity 100.0%; Pred. No. 1.2 Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 27-UN.1997

ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27.026

REFERENCE/DOCKET NUMBER: 48466-342

TELECHONE: 617-523-3400
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; Sequence 65, Application US/08776971B
; Patent No. 6228984
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; Kawamata, Yugo
                                                                                                                                                                                                                                                                  Sequence 47, Application US/09105678A
Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pi
Matches 19; Conservative 0;
                                                                                                                          1 TPDINPAWYASRGIRPVGR 19
                                                                                                                                                           1 TPDINPAWYASRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPDINPAWYASRGIRPVGR 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: peptide US-09-105-678A-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 21 amino TYPE: amino acid
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US-09-560-915-18
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Gaps

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Kawamata, Yuji
Hosoya, Masaki
Fusui, Roji
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 99.1%; Score 107; DB.3; Length 22; I Similarity 100.0%; -Pred. No. 1.4e-10; 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/08/776,971B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION SOURCES APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28 DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 18-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-A040-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-8-8-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
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NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 471
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPDINPAWYASRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TPDINPAWYASRGIRPVGR 19
                           REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 484
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                     27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-523-64
INFORMATION FOR SEQ ID NO: 66
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-105-678A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -08-776-971-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 19
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patent No. 6103882

GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE. PPONTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

99.1%; Score 107; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                   MEDIUM TYPE: Floppy disk Compatible COMPUTER: IEM PC compatible COPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PALENTIN PELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208 FILING DATE: 26-JUN-1998 FILING DATE: 26-JUN-1998 FILING DATE: 26-JUN-1998 APPLICATION NUMBER: US/09/105,678 FILING DATE: 26-JUN-1997 ATCRNEY/AGENT INFORMATION: NAME: COALIN, DATE: 37,026 REGISTRATION NUMBER: 27,026 REGISTRATION NUMBER: 27,026 REGISTRATION NUMBER: 27,026 REGISTRATION NUMBER: 27,026 REGISTRATION NUMBER: 37,026 RE
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MEDIUM TYPE: Floppy disk
COMPUTER: ELB PC compatible
COPEDATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
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130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-421-208-47
                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid STRANDEDNESS:
                                                         MA
USA
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CITY: Boston
                                 Boston
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COUNTRY: US
ZIP: 02109
                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.1%; Score 107; DB 3; Length 22; Best Local Similarity 100.0%; Pred. No. 1.4e-10; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Suchaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Pc-DoS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE: 26-JUN 1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 26-JUN 1998
APPLICATION NUMBER: UP 172118/1997
ATTORNEY/AGENT INFORMATION:
NAME: COLIN, DATE G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 37,026
REGISTRATION NUMBER: 37,026
REGISTRATION NUMBER: 27,026
REFERRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
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                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-08-776-971-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 48, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
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                                                                                                                         STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
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Matches 19; Conserv
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US-09-421-208-48
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TPDINPAWYASRGIRPVGR 19

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Gaps
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| Sequence 43. Application US/09105678A
| Patent No. 6103892
| GENERAL INFORMATION:
| APPLICANT: Suenaga, Masato
| APPLICANT: Moriya, Takeo
| APPLICANT: Tanaka, Yoko
| APPLICANT: Moriya, Takeo
| TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
| NUMBER OF SEQUENCES: 52
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
| STREET: 130 Water Street
| CITY: Boston
| STATE: MA
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 3; Length 31;
Pred. No. 2e-10;
0; Mismatches 0; Indels
Sequence 9, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:
APPLICANT: Submaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: SEQUENCES:
CORRESPONDENCE SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                         CZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
RETERRENCE/DOCKET NUMBER: 27,026
RETERRENCE/DOCKET NUMBER: 37,026
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION PROPERTION:
TELECOMMUNICATION PROPERTION:
TELEPRAX: 617-523-3400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHRARACTERISTICS:
TENTORNEY 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%; Sco.
100.0%; Pre
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Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                             STREET: 130 W
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
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US-09-105-678A-43
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09421208
| Patent No. 6288561
| GENERAL INFORMATION:
| APPLICANT: Suenaga, Masato
| APPLICANT: Moriva, Takeo
| APPLICANT: Nishimura, Osamu
| TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LICAND
| NUMBER OF SEQUENCES: 5.2
| CORRESPONDENCE ADDRESS: 5.2
| ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
| STREET: 130 Water Street
| CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDITOM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: US/09/105,678
FILING DATE: 27-UN-1997
ATTONNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: COALIN, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein FRAGWENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPDINPAWYASRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 TPDINPAWYASRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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STATE: MA
COUNTRY: US/
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-776-971-61
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Hosoya, Masaki
Fujii, Masaki
Fujii, Shoji
Ritada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
CORRESPONDENCE: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LL.P
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

99.1%; Score 107; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                      MEDIUS. ...

COMPUTER: IBM PC compatile
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SUSTING SYSTEM: PC-DOS/MS-DOS
SUSTING SPELICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/109/12118/1997
FILING DATE: 27-JUN-1997
ATTONEY/AGENT INFORMATION:
NAME: COALIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
TELEFRAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 06-F65-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
PPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
                                                                 Eloppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 61, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 TPDINPAWYASRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide US-09-105-678A-43
                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Habata,
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US-09-4212-1208-43

Detent No. 625561

FREAL INFORMATION: Masato
APPLICANT: Montry, Takeo
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19F2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE SEE
CORRESPONDENCE SEE
CORRESPONDENCE SEE
CORRESPONDENCE SEE
CORRESPONDENCE SEE
CORRESPONDENCE SEE
STREET: 130 Water Street
STREET: D310 Water Street
STREET: D310 Water Street
STREET: D310 Water Street
CONDITY: BOSCON
STREET: D409

CONDITY: BOSCON
STREET: BASCON
STREET: BASCON
STREET: BOSCON
STREET: BASCON
STREET: BASCON
STREET: BOSCON
STREET:
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Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                             Query Match 99.1%; Score 107; DB 3; Length 31; Best Local Similarity 100.0%; Pred. No. 2e-10; Matches 19; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 TPDINPAWYASRGIRPVGR 30
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                                                                                                                                                                                                                                                                                                                                                          1 TPDINPAWYASRGIRPVGR 19
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-421-208-43
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 12, 2004, 14:37:36; Search time 8.83721 Seconds (without alignments) 217.697 Million cell updates/sec

US-09-700-643A-12 110 1 TPDINPAWYAGRGIRPVGRX 20

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

a	Description	~		14	hypothetical prote	hypothetical prote	poth		ഗു		hypothetical prote			ical prot		synt	7		probable aldehyde	glut	hypothetical prote	hypothetical prote	VirB6 type IV secr	fructose-bisphosph	sensory protein ki	amino	probable inner mem	brane t	lar pro	cvtochrome P450 1A
SUMMAKIES	ID	JC7607	AH3166	0069	3317	T47959	F83376	H82852	B38176	T49717	A87664	F71015	AB1034	T21969	S11210	G82844	C84780	H83396	F83142	29	081	237	535	407	022	472	9062	854	219	S
	DB	. ~	~	-	~	7	N	~	~	~	~	7	~	~	N	N	N	~1	~	~	7	~	N	~	~	7	7	(7	N	C
	Length	83	419	430	527	790	664	333	424	779	226	284	424	767	798	390	398	506	506	220	276	309	313	359	399	476	476	476	503	
ex	Query		47.3	9		44.5		ä	Н	41.4	0	40.9	0	0	0	0	0	ത	σ	σ	O)	σ	σ	σ	σ	σ	σ	39.1	O	σ
	Score			51				4	46	45.5	4	4.5	45	4	45	44	44		m	4	43	43		43	43	43	43	43	43	43
	Result No.	)   H	. 6	m	4	ın	v	7	œ		10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	c

hypothetical prote	fusion, PTS system	hypothetical prote	probable magnesium	probable transposa	hypothetical prote	cytochrome-c oxida	Lyth homolog (impo	conserved hypothet	probable transport	probable transport	hypothetical 41.1K	pyruvate dehydroge	peptidoglycan-bind	tubulin beta chain	nitrite extrusion
T47548	H96951	C84480	T31462	T36978	A75117	266600	E87151	B87507	F91173	F86019	S47704	F81694	H87660	S18597	C83160
~	N	N	N	N	7	0	0	N	0	~	~	~	N	0	0
548	627	938	1292	143	284	311	335	352	375	375	375	428	433	453	468
39.1	39.1	39.1	39.1	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2	38.2
43	43	43	43	42	42	42	42	4	42	42	4.2	42	42	42	42
30	31	32	33	34	52	36	3.7	80	6	40	4	42	43	44	45

## ALIGNMENTS

RESULT 1 JG7607 JG7607 JG7607 JG7607  JG7607  Drolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001 C;Accession: JG7607 R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T. B;Ochem. Biophys. Res. Commun. 281, 53-55, 2001 A;Tile: Isolation and characterization of the rat prolactin-releasing peptide gene: Mul A;Tile: Isolation and characterization of the rat prolactin-releasing peptide gene: Mul
 A,Contents: Spleen A,Contents: Spleen A,Accession: JC7607 A,Cross-references: DBBJ:AB040612; DDBJ:AB040613 A,Cross-references: DBBJ:AB040612; DDBJ:AB040613 A,Comment: This peptide induces arachidonic acid metabolite release from rat anterior places and stimulation of ACTH secretion from the pituitary. C,Genetics: A,Genetics: A,Genetics: A,Genetics:
 Query Match Best Local Similarity 94.7%; Pred. No. 4.9e-09; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AH3166
hypothetical protein ugpB [imported] - Agrobacterium tumefaciens (strain C58, Dupont) p)
hypothetical protein ugpB [imported] - Agrobacterium tumefaciens
C;Space: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AH3166
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Wonks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 244, 2317-2323, 2001
S;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Attle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Accession: AH3166
A;Accession: AH3166
A;Accession: AH3165
A;Accession: L419 < XUN>
A;Accession: L419 < XUN>
A;Coss-references: GB:AE008687; PIDN:AAL45750.1; PID:g17743483; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: ugpB

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hypothetical protein F15G16.60 - Arabidopsis thaliana
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiAccession: T47959
Ribe Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet, Submitted to the Protein Sequence Database, January 2000
A;Reference number: 224480
A;Accession: T47959
A;Accession: T47959
A;References: preliminary
A;Residues: 1-790 cDEE:
A;Cross-references: EMBL:AL132959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aritle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogarkeference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83376
A;Accession: F83376
A;Accession: Praininary
A;Molecule type: DNA
A;Residues: 1-664 <5TO-
A;Estidues: 1-664 <5TO-
A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN001;
A;Experimental source: strain PA01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (strain PA01) ("Species: Pseudomonas aeruginosa ("Species: Pseudomonas aeruginosa ("Species: IS-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 ("Spacession: F83376 "Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                      A, Experimental source: cultivar Columbia, BAC clone F15G16
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Pred. No. 18;
2; Mismatches
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62.5%; Pred. No. 18;
ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: 3
A,Introns: 39/1; 678/2; 698/3; 773/2
A,Note: F15G16.60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 PPHNPRTYGSRGLOPHGR 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.5%;
50.0%;
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Best Local Similarity 50.0°
Matches 9; Conservative
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Best Local Similarity 62.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                 RESULT 3
B69009
conserved hypothetical protein MTH1070 - Methanobacterium thermoautotrophicum (strain De C;Species: Methanobacterium thermoautotrophicum
C;Species: Description 1999 #sequence_revision 29-Jan-1999 #text_change 23-Jul-1999
C;Accession: B69009
R;Smith, D.R.; Doucette-Stamm, D.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Cju, D.; Spadefora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Recession: B69009
A;Status: nucleic acid sequence not shown; translation not shown
A;Rocession: B69009
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-430 cMTH>
A;Cross-references: GB:Ab000877; GB:AE000666; NID:g2622157; PIDN:AAB85559.1; PID:g262216
A;Sqantics:
A;Gene: MTH1070
C;Superfamily: conserved hypothetical protein MTH1070
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A;Experimental source: strain Bristol N2; clone C24G6
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Mypotherical protein C24G6.6 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Sacession: T33175
R,Gcco, T.; Bradshaw, H.; Keppler, D.
R,Gcco, T.; Bradshaw, H.; Keppler, D.
R,Description: The sequence of C. elegans cosmid C24G6.
A,Reference number: Z21298
A,Accession: T33175
A,Status: T23175
A,Status: preliminary; translated from GB/EWBL/DDBJ
A,Residues: J-227 «GRE»
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                                                  47.3%; Score 52; DB 2; Length 419; larity 36.8%; Pred. No. 3.2; Conservative 5; Mismatches 7; Indels
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Pred. No. 8.2;
2; Mismatches 2
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A;Gene: CESP:C24G6.6
A;Map position: 5
A;Introns: 20/3; 77/1; 129/2; 208/3; 470/2
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323 SPEANATWFAGTGYLPINK 341
                                                                                                                                                1 TPDINPAWYAGRGIRPVGR 19
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Best Local Similarity 66.7%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 DINPAWYAGRGIR 15
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                     Query Match
Best Local Similarity
7; Conserva
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tes 9; Conserv
A; Genome: plasmid
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Best Local S
Matches
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A;Status: preliminary A;Molecule type: DNA A;Residues: 1-333 <SIM>

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A,Molecule type: DNA
A,Residues: 1-779 <SCH>
A,Cross-references: ENRL:AL356172; GSPDB:GN00116; NCSP:B23121.300
A,Experimental source: BAC clone B23121; strain OR74A
C,Genetics:
A,Gene: NCSP:B23121.300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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A;Cross-references: GB:AE003860; GB:AE003849; NID:g9104830; PIDN:AAP82881.1; GSPDB:GN001 A;Cross-references: strain 9a5c
B;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Bartones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Briones, M.C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm O.D.; Junqueaira, M.L.; Remper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuizamae, E.E.; Laigy chado, M.A.; Madeira, A.M.B.N.; Madeira, H.W.; Martuno, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Ollveira, M.A.; de Ollveira, M.C.; de Ollveira, R.C.; Palmieri, D.A; Adithors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., M.A.; da Silva; A.A.; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SamB protein - Salmonella typhimurium
Cispedies: Salmonella typhimurium
Cispedies: Salmonella typhimurium
Cispedies: Salmonella typhimurium
Cipacession: B38176
Rivohmi, T.; Hakura, A.; Nakai, Y.; Matanabe, M.; Murayama, S.Y.; Sofuni, T.
J. Bacteriol. 173, 1051-1063, 1991
A;Title: Salmonella typhimurium has two homologous but different umuDC operons: cloning
A;Reference number: A38176; MUID:91123176; PMID:1991707
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R,Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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N,A1ternate names: protein B23L21.300
C,Species: Neurospora crassa
C,Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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A;Cross-references: GB:D90202; NID:g217087; PIDN:BAA14226.1; PID:g217089
A;Experimental source: strain LT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.8%; Score 46; DB 2; Length 333; 53.3%; Pred. No. 21; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: restores UV mutability; involved in mutagenesis C;Superfamily: umuC protein C;Keywords: DNA repair; induced mutagenesis; SOS mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: XFO068
C;Superfamily: 4-hydroxybenzoate octaprenyltransferase
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Best Local Similarity 53.5%
Local Similarity 53.5%
Local Similarity 53.5%
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A;Accession: T49717
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Best Local Similarity
Matches 8; Conserv
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hypothetical protein CC3347 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: A67664
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; DoBoon, R.T.; DoBoon, R.T.; DoBoon, R.T.; DoBoon, R.T.; DoBoon, M. L.; Haft, D.H.; Kolor
In, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Telle: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: F71015
B;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir M.; Offuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. S, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUD:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
A,Residues: 1-284 <KAW>
A)Cross-references: GB.AP000006; NID:g3236133; PIDN:BAA30526.1; PID:g3257843
A,Experimental source: strain OT3
A,Note: this accession replaces an interim accession for a sequence replaced by GenBank
C,Genetics:
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A)Cross-references: GB:AE005673; NID:g13425049; PIDN:AAK25309.1; GSPDB:GN00148
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                               3;
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DB 2; Length 779;
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C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.9%; Score 45; DB 2; Length 226; 50.0%; Pred. No. 20; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.9%; Score 45; DB 2; Length 284; 50.0%; Pred. No. 26; cive 3; Mismatches 6; Indels
                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein PH1420 - Pyrococcus horikoshii
41.4%; Score 45.5; DB
58.8%; Pred. No. 59;
tive 1; Mismatches
                                                                                                                                                                                             286 TDYLNPATRRWYANRGI 302
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                                                                                                                              1 TPDINPA---WYAGRGI 14
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125 VNPDWRSGRALRDV 138
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Best Local Similarity 50.00
For 7; Conservative
   Query Match
Best Local Similarity 58.8 Matches 10; Conservative
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Best Local Similarity 50.0%
Matches 9; Conservative
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A, Contents: annotation
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A;Molecule type: DNA
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Matches
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                                                                                                                      UV protection protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (st CiSpecies: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi (st C;Species: OS-Nov-2001 #sequence_revision O9-Nov-2001 #text_change 18-Nov-2002 C;Accession: AB1034 R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T., Connetron, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Monle, S.; O'Gaora, P.
Nature 413, 4848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova; A;Accession: AB1034
A;Accession: AB1034
A;Accession: AB1034
A;Accession: AB1034
A;Accession: AB1034
A;Residues: 1-424-CPAR>
A;Gross-references: GB:AL513382; PIDN:CAD06719.1; PID:g16505372; GSPDB:GN00176
C;Genetics: A;Gene: samB
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A,Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1;
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Submitted to the EMBL Data Library, January 1996
A;Reference number: 219495
A;Recession: T21969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-767 «WIL»
A;Residues: 1-767 «WIL»
A;Residues: 1-767 «WIL»
A;Residues: clone F38E11
C;Genetics:
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|Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
|Accession: T21969
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C;Species: Rattus norvegicus (Norway rat)
C;Jate: 21 - Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C;Accession: S11210
R;Jōffers, M.; Paciucci, R.; Pellicer, A.
Nucleic Acids Res. 18, 4891-4899, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F39E11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #Fev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
217 PYIEPTFYALRGLELLGR 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747 PDVKPAWY 754
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                                                                              RESULT 12
AB1034
UV, protect
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A, Residues: 1.390 <51NA
A, Cross-references: GB:AE003866; GB:AE003849; NID:g9104906; PIDN:AAF82941.1; GSPDB:GN001.
A, Cross-references: GB:AE003866; GB:AE003866; BLDN:AAF82941.1; GSPDB:GN001.
A, Experimental source: strain 9a5c
Briones, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. S-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 200
A, A.A. Franca, S.C.; Franca, C.C.; Franca, C.C.; Franca, C.C.; Franca, C.C.; Franca, C.C.; Franca, J.D.; Kraijana, J.D.; Krieger, J.E.; Marques, D.C.; Franca, C.C.; Marques, M.L.; Kemper, E.L.; Ktaijana, J.D.; Krieger, J.E.; Marcios, E.C.; Myastins, E.C.; Franca, M.A.; Madeira, H.M.F.; Marcio, C.L.; Marques, M.V.; Marcins, E. F.G.; Nunes, L.R.; Oliveira, M.A.; Madeira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de N.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Aluthors, da Silva, A.M.; Silva Jr., W.A.; da Silvaira, M.; Tauhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A. Reference number: A.S.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Objective synthase XF0128 [imported] - Xylella fastidiosa (strain 9a5c)
C,Species: Xylella fastidiosa
C,Species: Xylella fastidiosa
C,Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C,Accession: G92844
R,anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 2000
A,Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Reference number: A82515; MUID:20365717; PMID:10910347
A,Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A,Title: Characterization of unr; a gene closely linked to N-ras.
A,Reference number: S11210; MUID:90370473; PMID:2204029
A,Accession: S11210
A,Molecule Lype: mRNA
A,Residues: 1-798 «AEF»
A,Cross-references: EMBL:X52311; NID:g57454; PIDN:CAA36549.1; PID:g57455
C,Keywords: DNA binding
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                                                                                                                                                                                                                                                                                                                    Length 798,
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                                                                                                                                                                                                                                                                                                                            40.9%; Score 45; DB 2;
47.1%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
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Best Local Similarity 47.13
Best Local 8; Conservative
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nes 7; Conservative
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August 12, 2004, 14:37:35 ; Search time 5.23256 Seconds (without alignments) 199.024 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                     141681 seqs, 52070155 residues
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                             US-09-700-643A-12
110
1 TPDINPAWYAGRGIRPVGRX 20
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

141681

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	os tau	rattu		coryn		Ø		rattus						E			Н		streptomy		Q46306 clostridium	pseudomona				methano	yersinia p	limu	limu	gall	Q9uq49 homo sapien	homo	Enm
ΩI	PRRP BOVIN	PRRP_RAT	PRRP HUMAN	EX7L_COREF	EX7L_CORGL	EX7L_STRCO	SAMB_SALTY	UNR RAT	CYCE CHRVI	ALF HAEIN		CP12 CANFA	TRA2 DROVI	ISPH_MYCLE	YHHJ_ECOLI	TBB2 GEOCN		NRP1_YEAST	GLGB_STRAW	ARGC_BACHD	TETP_CLOPE	GIDB_PSESM	HEM6 RALSO	SPEB_STRCL	Y762 METJA	Y576_METJA	ALR1_YERPE	OPS1_LIMPO	OPS2_LIMPO		NER3 HUMAN	ATR2 HUMAN	ATR1_MOUSE
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Score	01	105	0	S	52	46	46	45	44	43	43	43	42	42	42	42	42	42	4.2	41.5	ä	41	41	41	41	41	41	41	41	41	41	41	41
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Q9h6x2 homo sapien P47069 saccharomyc	P18302 gallus gall Q9h078 homo sapien	P11528 arbacia pun Q9x079 thermotoga	075369 homo sapien Q80x90 mus musculu	P43268 homo sapien Q9jn46 rhodobacter	P53281 saccharomyc Q9ryd4 deinococcus
ATRI HUMAN YJB9 YEAST	DREB_CHICK SKD3_HUMAN	CYGR ARBPU Y984 THEMA	FLNB_HUMAN FLNB_MOUSE	ETV4_HUMAN AAM1_RHOSH	YG3D_YBAST NPD_DEIRA
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564	652 707	986 1536	2602	551	241 246
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34	3 3 6	388	4 4 0 4	44	44.0

## ALIGNMENTS

PRT; 98 AA.	30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 28-REB-2003 (Rel. 41, Last annotation update)	·H	chordata. Cranista. Verrebrata: Riteleostomi:	Chordata, Ciantata, Vertebrata, Ductrootomis, Cetartiodactyla, Ruminantia, Pecora, Bovoidea;		SECHENCE OF 23-52.		*	osoya M., Fukusumi ekiguchi M.,	Kurokawa T., Nishimura O., Onda H., Fujino M.;	eptide in the brain.";	se and regulat	expression of prolactin through its receptor GPR10. May stimulate	lactotrophs directly to secrete PKL. TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.	1 The second sec	This SWISS-PROF enery is copyright. It is produced through a correspondence. The Swiss Institute of Bioinformatics and the EMBL outstation -	the European Bioinformatics Institute. There are no restrictions on its	t institutions as long as its content is in no way actionant is not removed insace by and for commercial	se http://www.isb-sib.ch	ő		al; Cleavage on pair of basic residues.	100000 BOINGOO CATORETER ATTENDED			AMIDATION (G-54 PROVIDE AMIDE GROUP).		Score 109; DB 1; Length 98; ; Pred. No. 4.2e-10;	0; Mismatch
ANDAR	(Rel. 39, Creat (Rel. 39, Last (Rel. 41, Last	FIGURE TO TELEGISTING FORTER HORMONE) [Contains: Prolac Teleasing peptide PrRP20].	•		inae; Bos. 913;	[1] SECTIENCE FROM N.A. AND SECTIENCE OF		MEDLINE=98268781; PubMed=9607765;	abata Y., Fuj asuo Y., Asan	Nishimura O.	-releasing pe	72-276(1998). : Stimulates	on of prolact	phs directly PECIFICITY: M		KOľ entry is Swiss Instit	Bioinformati	-profit inst	requires a license	mail to licen	EMBL: AB015417; BAA29025.1;	Amidation; Signal;		23 53		23	8 AA; 10544 MW	n Similarity 100.0%	vat
1 DVIN RRP BOVIN 81264;	30-MAY-2000 30-MAY-2000 28-FEB-2003	rotactin-red hormone) (Cor releasing per	Bos taurus (Bovine)	Eukaryota; Metazoa; Mammalia; Eutheria;	Bovidae; Bovinae; NCBI_TaxID=9913;	[1] SECHENCE SEC	TISSUE=Brain;	MEDLINE=9826	Hinuma S., Ha	Kurokawa T.,	"A prolactin	Nature 393:27	expression	lactotroj -!- TISSUE SI		This SWISS-P.	the European	use by non-profit	entities req	or send an e	EMBL: AB0154	Hormone; Ami	SIGNAL	PEPTIDE	PROPER	S	SEQUENCE 9	Query Match Best Local Simi	19;
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RESULT 2

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D0C75A264EEE4F29 CRC64;
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                                                                                                                                                                        Conservative
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es 18; Conserv
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P81277;
                                                         SEQUENCE
                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN=Sprague-Dawley, TISSUE=Hypothalamus;
Anderson S.T., Kokay, I.C., Lang T., Grattan D.R., Curlewis J.D.;
"Quantitation of prolactin-releasing peptide (P.RP) mRNA expression in specific brain regions during the rat cestrous cycle and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPDINPAWYTGRGIRPVGRFGRRRATPRDVTGLGQLSCLPL
DGRTKFSQRG -> SECLTYGKQPLTSFHPFTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor.";
Regul. Pept. 83:1-10(1999).
-!- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactorrophs directly to secrete PRL.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116,
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                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98268781; PubMed=9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
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TISSUE SPECIFICITY: Widely expressed, with highest levels in medulla oblongata and hypothalamus.
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PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
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EMBL; AF521290, AAM82154.1; -.
PIR; JC7607; Signal; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-59426652; Pubwed=10498338;
Fujil R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hir
Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                      83 AA
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                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                releasing peptide PrRP20]
                                                      STANDARD;
                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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SIGNAL 1 21
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               PRRP_RAT
ID PRRP_RAT
AC P81278; Q8K3Y0;
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-!- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.

-!- TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.
                                                                               Gaps
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31, Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=99426652; PubMed=10498338; Rawamata Y., Habata Y., Hinuma S. Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S. Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sumino Y., Fujino M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCPI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION (G-54 PROVIDE AMIDE GROUP) 229A2F3F50CF981B CRC64;
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PROLACTIN-RELEASING PEPTIDE PRRP20.
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0
Score 105; DB 1; Length 83;
Pred. No. 1.5e-09;
); Mismatches 1; Indels
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Pred. No. 3.2e-09;
0; Mismatches 1; Indels
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COREF

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28-FEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
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                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
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                                                              (Exonuclease VII large subunit). XSEA OR CGL1025.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 13:1572-1579(2003).

-!- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity).

-!- GATALNITY: Expuncheolytic oleawage in either 5' to 3'-
or 3'- to 5'-direction to yield nucleoside 5'-phosphates.

-!- SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.,
                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Nuclease; Exonuclease; Complete proteome. SEQUENCE 413 AA; 45171 MW; D3BABD9687C6EESD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULĀR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 1;
Pred. No. 1.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 41, Created)
(Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP005217; BAC17888.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; Mr_00378; -; 1.
InterPro; IPR003753; Exonuc VII L.
InterPro; IPR008994; Nucleic_acid_OB.
Pfan; PP02601; Exonuc VII L; 1.
TIGRFAMS; TIGR00237; XeeA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAFYAGRGSFSLWVTDIRPVG 110
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                                              1 TPDINPAWYAGRGIRPVGR 19
                                                                                                 34 TPDINPAWYASRGIRPVGR 52
                                                                                                                                                                                                                                                                                                                                                                                                                       (Exonuclease VII large subunit)
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efficiens.";
------ Res. 13:1572-1579(2003)
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium efficiens.
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Best Local Similarity 57.1'
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=152794;
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EX7L_CORGL
ID EX7L_CORGL
AC Q8NRM3;
DT 28-FEB-2003 (
                                                                                                                                                                                                                                                       COREF
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                                                                                                                                                                                                                                                                         "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.", "Complete genomic sequence of Coryneback/DDB databases.
Submitted (MAY-2002) to the EMBL/GenBank/DDB databases.
-!- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity).
-!- CATALYTIC ACTIVITY: Exomocleotytic cleavage in either 5' to 3'-
Or 3' to 5'-direction to yield nucleoside 5'-phosphates.
-!- SUBUNIT: Heterooligomer composed of large and small subunits (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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28-PEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
               Bacteria, Actinobacteria; Actinobacteridae, Actinomycetales; Corynebacterineae; Corynebacterineae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 1; Length 417; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBLI, ALCONOS, -, 1.
HAMAP, MF 00178; -, 1.
INTERPRO, IPRO03753; Exonuc_VII_L.
INTERPRO, IPRO08994; Nucleic_acid_OB.
Pfam; PF02601; Exonuc_VII_L; 1.
TIGRFAMB; TIGR00237; xseA, 1.
Hydrolase; Nuclease; Exonuclease; Complete proteome.
crontence 417 AA; 45582 MW; B32CD9286C173C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the xseA family.
Corynebacterium glutamicum (Brevibacterium flavum).
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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MEDLINE=90370473; PubMed=2204029;
Jeffers M.,
Jeflucci R., Pellicer A.;
"Characterization of unr, a gene closely linked to N-ras.";
"Characterization of unr, a gene closely linked to N-ras.";
Nuclet. Acids Res. 18:4891-4899(1990).
-!- FUNCTION: RNA-binding protein (By similarity).
-!- SUBCELIGIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the cold-shock domain (CSD) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 1; Length 424; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                      FF8C47476CC58A2B CRC64;
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CSD 2 (INCOMPLETE).
CSD 3.
CSD 4 (INCOMPLETE).
CSD 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      798 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                             EMBL, D90202; BAA14226.1; -.
PIR, B38176, B38176.
PAMAP, MF 01113; atypical; 1.
InterPro; IPR001126; UMUC_like.
PEdm; PF00817; IMS; 1.
PROSITE; PS50173; UMUC; 1.
Plasmid; SOS mutagenesis; DNA_repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X52311, CAA36549.1; -.
PIR, S11210; S11210.
HSSP, P1277; IMJC.
InterPro; IPR002059, Cold shock.
InterPro; IPR008994; Nucleic_acid_OB.
Pfam; PF00313; CSD; 7.
                                                                                                                                                                                                                                                                                                                                                                DME
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SMART; SM00357; CSP; 5.
RNA-binding; Repeat.
26 87 CSD
                                                                                                                                                                                                                                                                                                                                                                                      424 AA; 47727 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        41.8%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 PGKGKIWFÄGRGIAP 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136
136
297
349
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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DOMAIN
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          THE HEAVE BEEN AND THE STATE OF THE STATE OF
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                                                                                                                                                                     -:- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity).
-:- CATALYTIC ACITYLY: Exonucleolytic cleavage in either 5' to 3'- or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
-:- SUBNNIT: Heterooligomer composed of large and small subunits (By
                          Taylor K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                          Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                             "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).", Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid 60-mDa cryptic.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Salmonella typhimurium has two homologous but different umuDC operons: cloning of a new umuDC-like operon (samAB) present in a 60-megadalton cryptic plasmid of 8. typhimurium.";
J. Bacteriol. 173:1051-1063(1991).
-!- FUNCTION: Involved in UV protection and mutation.
-!- SIMILARITY: Belongs to the DNA polymerase type-Y family.
-!- SIMILARITY: Contains 1 umuC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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  Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.8%; Score 46; DB 1; Length 402; 47.6%; Pred. No. 9.8; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91123176; PubMed=1991707;
Nohmi T., Hakura A., Nakai Y., Watanabe M., Murayama S.Y.,
Sofuni T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP, MF_00378; -; 1.
InterPro; IPR003753; Exnuc VII_L.
InterPro; ORNO04365; tRNA_anti.
Pfam; PF0136; tRNA_anti.
IGREAMS; TIGR00237; xesA; 1.
ITGREAMS; TIGR00237; xesA; 1.
Hydrolase; Muclease; Exonuclease; Complete protecme.
SEQUENCE 402 AA; 43882 MW; 145929A8372B4E08 CRC64;
                                                                                                                                                                                                                                                                                                                        similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the xseA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 47.6
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                                                                          Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SamB protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPROJ IPRO0155, CytC heme BS.

INTERPRO; IPRO0158; CytC RC.
Pfam, PF02276; CytC RC;
Prop. PF00101; CytC RC;
PRODOM; PF010011; CytC RC;
PRODOM; PF010011; CytC RC;
PROSTIE; PS00190; CYTOCHROWE C;
PROSTIES CYTOCHROWE C;
PROSTIES CYTOCHROWE CYTOCHROWE CYTOCHROWER CYTOCHROWER CYTOCHROWERE 
                                                                                                                                                                               Gaps
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-: SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (By similarity).
-: PTM: Binds 4 here groups per molecule.
-: SIMILARITY: HIGH, WITH OTHER PHOTOSYNTHETIC REACTION CENTER CYTOCHROME C SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERAINE FROM N.A.
SERAINE FROM N.A.
SERAINE FROM N.A.
CORSON G.E., Nagashima K.V., Matsuura K., Sakuragi Y., Ruwanthi W.,
COLSON G.E., Nagashima K.V., Matsuura K., Sakuragi Y., Ruwanthi W.,
COLSON H., Allen R., Knaff D.B.;
"Primary structure of genes encoding light-harvesting and reaction
center proteins from Chromatium vinosum ";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE REACTION CENTER OF PURPLE BACTERIA CONTAIN A
TIGHTLY BOUND CYTOCHROME MOLECULE WHICH RE-REDUCES THE PHOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
N-palmitoyl cysteine (By similarity).
IRON (HEME 1 AXIAL LIGAND)
(BY SIMILARITY).
HEME 1 (COVALENT) (BY SIMILARITY).
HEME 1 (COVALENT) (BY SIMILARITY).
                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Photosynthetic reaction center cytochrome C subunit precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Protecobacteria; Gammaproteobacteria; Chromatiales;
Chromatiaceae; Allochromatium.
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S-diacylglycerol cysteine (By
                                                                                                                                  40.9%; Score 45; DB 1; Length 798; 47.1%; Pred. No. 26;
                                                                                                                                                                               Indels
                                                                                          F484B3FA8B0995A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    383 AA
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  CSD 6.
CSD 7.
CSD 8.
CSD 9.
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                                                                                                                                                                                                                                                      88894 MW;
                                                                                                                                                                                                                            1 TPDINPAWYAGRGIRPV 17
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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798 AA;
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                                                                                                                                                            Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1049;
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082947;
                                                                       DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Rd / KW20 / KW20
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-!- CATALTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
-!- COFACTOR: Zinc (By similarity).
-!- PATHNAX: Glycolysis; sixth step.
-!- PATHNAX: Glycolysis; sixth step.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBUNIT: Belongs to class II fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (COVALENT) (BY SIMILARITY).
4 (COVALENT) (BY SIMILARITY).
(HEME 4 AXIAL LIGAND)
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                 (BY SIMILARITY)
(BY SIMILARITY)
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(BY SIMILARITY)
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IRON (HEME 1 AXIAL LIGAND)
(BY SIMILARITY).
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96BCD91FF1B9AE7E CRC64;
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19;
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28-FEB-2003 (Rel. 41, Last annotation update)
Fructose-bisphosphate aldolase (EC 4.1.2.13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44;
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263 TPQRTTAWYAIRHVRDINQ 281
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01-NOV-1995 (Rel. 32, Last seqn
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 AA; 41522 MW;
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Best Local Similarity
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METAL
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ALF HAREIN
10 1-NO
DT 28-FB
DD 01-NO
DT 28-FB
DD 01-NO
DD 28-FB
DD 01-NO
DD 02-NO
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51662 MW;

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Pfam; PF01235; Na Ala symp; 1.
PRINTS: RR00175; NALASMPORT.
TIGREAMS: TIGRO0335; agc5; 1.
PROSITE; PS00873; NA ALANINE SYMP; 1.
Hypothetical protein; Transmembrane; Inner membrane; Transport;
                              EMBL; AE00011; AC73118.1; -.
PIR; G64720; G64720.
Ecodene; EG1155; yaa.
InterPro; IPR002233; AA/rel_permeasel.
InterPro; IPR001463; Na/Ala_symport.
                                                                                                                                                                                        Complete proteome.
                   D10483; BAB96585.1;
                                                                                                                                                                                                                                                                                                                                        414
476 AA;
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203
233
300
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P56592;
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TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=KIZ / MG1655,

MEDINE=97426617; PubMed=9278503;

MEDINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

Mau B., Shao Y.;

"The Complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).

- SUBCELLUTAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Sason K., Mizobuchi K., Nakata A.; "Systematic sequencing of the Escherichia coli genome: analysis of the 0-2.4 min region.", Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential).
-!- SIMILARITY: BELONGS TO THE SODIUM:ALANINE SYMPORTER FAMILY (SAF). STRONG, TO H.INFLUENZAE H10183.
                                                                                                                                                                                                                                                                                                       39.1%; Score 43; DB 1; Length 359; 70.0%; Pred. No. 26; tive. 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         359 AA; 39339 MW; 1EDDFCDD0B69E32C CRC64;
                                                                                                   InterPro; IPR006411; Fruct bisp bact.
InterPro; IPR000771; K bp aldolase.
Pram, PF0116; F bp aldolase; 1.
ProDom; PF0002376; K bp aldolase; 1.
TIGRFAMS; TIGR00167; cbb3; 1.
TIGRFAMS; TIGR01520; PruBisaldo II A; 1.
PROSITE; PS00602; ALDOLASE CLASS II 1; 1.
PROSITE; PS00606; ALDOLASE CLASS II 2; 1.
Lyase; Glycolysis; Zinc; Complete profesome.
METAL 108 108 ZINC (BY SIMILARITY).
METAL 111 111 ZINC (BY SIMILARITY).
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1D YANJ ECOLI

AC 930143.

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 28-FEBS-2033 (Rel. 41, Last annotation update)

BD WAAJ OR B0007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92334977; PubMed=1630901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae, Escherichia
                                             EMBL; U32734; AAC22182.1; -.
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70...
7; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                     |:||:||:|
67 AFYAGKGIKP 76
                                                                                                                                                                                                                                                                                                                                                                   7 AWYAGRGIRP 16
                                                         PIR; C64074; C64074.
HSSP; P11604; 1B57.
TIGR; H10524; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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SEQUENCE
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STRAIN=Beagle; TISSUE-Liver;
CSTRAIN=Beagle; TISSUE-Liver;
MEDLINE=89087526; PubMed=2910310;
A hota K., Motova M., Komori M., Miura T., Kitada M., Kamataki T.;
A novel form of cytochrome P-450 in beagle dogs. P-450-D3 is a low spin form of cytochrome P-450 but with catalytic and structural properties similar to P-450 but with catalytic and structural Biochem. Pharmacol. 38:91-96(1989).
II properties similar to P-450 but with catalytic and structural monoxygenases. In liver microsomes, this enzyme is involved in an monoxygenases. In liver microsomes, this enzyme is involved in an monoxygenases. In liver microsomes, this enzyme is involved in an of structurally unrelated compounds, including steroids, fatty acids, and xenoblotics.

C -1-CATALYIC ACIMITY: RH + reduced flavoprotein + O(2) = ROH +
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome P450 1A2 (EC 1.14.14.1) (CYPIA2) (DAH2) (Cytochrome P450-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Beagle; TISSUE=Liver;
MEDLINE=91042464; PubMed=2122230;
Uchida T., Komori M., Kitada. M., Kamataki T.;
"Isolation of cDNAs coding for three different forms of liver microsomal cytochrome P-450 from polychlorinated biphenyl-treated
                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                     .
9
                                                            39.1%; Score 43; DB 1; Length 476; 44.4%; Pred. No. 34; tive 2; Mismatches 2; Indels
POTENTIAL.
2F6EB2E12E126E63 CRC64;
                                                                                                                                                                                                                                                                                     511 AA
                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Pharmacol. 38:644-651(1990)
                                                                                                                                                                                  120 DVNGQFRGGPAWYMARGL 137
                                                                                                                                         3 DIN-----PAWYAGRGI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 9-511 FROM N.A.
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                           Local Similarity
es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9615;
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                                                                                                                                                                  PEGNOTOS, LL.,
REARY, SWOO360, RRW, 1.
REARY, SWOO360, RRW, 1.
REARY, SWOO360, RRW, 1.
REARY, SWOO360, RRW, II.
REARY SEXUAL differentiation; Spermatogenesis, RNA-binding,
KW Alternative splicing; Phosphorylation.
RW Alternative splicing; Phosphorylation.
RW Alternative splicing; Phosphorylation.
RT DOMAIN 26 98 ARG/SER.RICH (RRI DOMAIN).
FT DOMAIN 184 204 LINKER.
FT DOMAIN 205 272 ARG/SER-RICH (RS2 DOMAIN).
ARG/SER-RICH (RS2 DOMAIN).
RT ARABINGTON 225).
/FIId=VSP 005903.
                                                                                                                                                                                                                                                                                                                                                                    38.2%; Score 42; DB 1; Length 272; 52.6%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the ispH family
                                                                                                                     EMBL; U72682; AAB58113.1; -.
EMBL; U72682; AAB58112.1; -.
1719Ase; PBG00015686; Dvir\tra2.
InterPro; IPR0005694; RNA_rec_mot.
Pfam; PF00076; rrm; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                188 TP--TPGVYMGRPSRPLGR 204
                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISPH MYCLE
                                                                                                                                                                                                                                                                                                                                                                      Query Match
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0
-:- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
-:- TISSUE SPECIFICITY: Constitutively expressed in liver.
-:- INDUCTION: By polychlorinated biphenyl (PCB) in liver and kidney.
-:- SIMILARIY: Belongs to the cytochrome P450 family.
PIR: B37222; B37222.
INTERFY: JPR001128; Cytochrome P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: The RS2 (Arg/Ser-rich domain 2) and RNP-CS (ribonucleoprocean consensus sequence) domains are required for (ribonucleoprocean consensus sequence) domains are required for both male sterliity and female-specific dax splicing but the RS1 domain is dispensable (By similarity). PTM: Extensively phosphorylated on serine residues in the RS domain (By similarity). SIMILARITY: Contains 1 RNA recognition motif (RRM) domain. SIMILARITY: Belongs to the SR family of splicing factors.
                                                                                                                                                                                                       453 453 IRON (HEME AXIAL LIGAND) (BY SIMILARITY)
511 AA; 57505 MW; 200904C54F4B3CB7 CRC64;
                                                                                                                                                                                                                                                                              Gaps
                                                                                                   InterPro; Iffnow, Trans, Trans, Trans, Trans, Trans, PRINTS; PRO1683; EP450. 1.
PRINTS; PRO1683; EP450.
PRINTS; PRO1885; P450.
Oxidorseluctase; Monooxygenase; Electron transport; Membrane; Heme; Microsome; Endoplasmic reticulum.
Trans (HEME AXIAL LIGAND) (BY SIMILARI'
                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila virilis (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                Query Match
39.1%; Score 43; DB 1; Length 511;
Best Local Similarity 58.3%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   TRA2 DROVI STANDARD; PRT; 272 AA. 002008; 002009; 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A. (ISOFORMS 272 AND 225).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=002008-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transformer-2 sex-determining protein.
                                                                                                                                                                                                                                                                                                                                    121 SPDSGPVWAÁGR 132
                                                                                                                                                                                                                                                                                                          1 TPDINPAWYAGR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7244;
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
TRA2_DROVI
                                                                                                                                                                                                                                                                                                                                                                                                         8
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1,

5

6; Indels

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Destret D.U., Massive gene decay in the leprosy bacillus.", Nature 409:1007-1011(2001).

-! FUNDTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) (By similarity).

-!-CAPTALTITC ACTIVITY: Isopentenyl diphosphate + NAD(P)(+) + H(2)O = (E)-4-hydroxy-3-methylbut-2-en-1-yl diphosphate + NAD(P)H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21128732; PubMed=11234002;
Cole S.T., Esglmeier K., Parkhill J., James K.D., Thomson N.R.,
Cole S.T., Esglmeier K., Garnier T., Churcher C., Harris D.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Enown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
09X781;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
4-hydroxy-3-methylbut2-enyl diphosphate reductase (EC 1.17.1.2)
ISPH OR LYTB OR LYTB2 OR ML1938 OR MLCB1222.06C.
                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                  Corynebacterineae; Mycobacteriace; Mycobacterium.
NCBI_TaxID=1769;
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[3]
SEQUENCE FROM N.A.
SPECIES=S.flexmeri; STRAIN=301 / Serotype 2a;
SPECIES=S.flexmeri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
MEDLINE=22272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Iu W., Wang J., Liu H., Yang J., Zhang Y., Zhang Y., Zhang Y., Zhang Y., Zhang Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Yang H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 225-374 FROM N.A.
SPECIESES. CO11; STRAIN=K12;
MEDLINE=9225920; PubMed=8387990;
Zhao S., Sandt C.H., Feulner G., Vlazny D.A., Gray J.A., Hill C.W.;
"Rhs elements of Escherichia coli K-12: complex composites of shared and unique components that hac different evolutionary histories.";
J. Bacteriol. 175:2799-2808(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF 00191; -; 1.
InterPro; IPR001451; LytB.
Pfam; PF02401; LYTB; 1.
TIGRPAMS; TIGR00216; ispH lytB; 1.
ISOprene biosynthesis; Complete proteome; Oxidoreductase; NADP.
SEQUENCE 332 AA; 36225 MW; F2A82A06EEC35E13 CRC64;
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SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.2%; Score 42; DB 1; Length 332; 77.8%; Pred. No. 34; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THIS STANDARD; PRT; 374 AA.

AC P1931, P76703;

DT 01-0T1-1993 (Rel. 26, Created)

DT 01-0T1-1993 (Rel. 30, Last sequence update)

DT 01-0CT-1994 (Rel. 30, Last sequence update)

DT 01-0CT-1994 (Rel. 30, Last sequence update)

DT 15-MAR-2004 (Rel. 30, Last annotation update)

DE 15-MAR-2004 (Rel. 30, Last annotation update)

DE 16-MAR-2004 (Rel. 30, Last annotation update)

DE 17-MAR-2004 (Rel. 30, Last annotation update)

DE 18-MAR-2004 (Rel. 30, Last annotation update)

OS Shigalla flexneri.

OC Bacteriah coli, and

OX NCBI_TAXID=562, 623;

RN (1)

RN (1)

RN (2)

RN MEDLINE=24316500; PubMed=804162 D.L., Plunkett G. R. Analysis of the Escherichia coli genome. V. DNA R. Capida H.J., Burland V., Daniels D.L., Plunkett G. R. Medlingels Res. 22:2576-2586 (1994).

RN (2)

RN (2)

RN MEDLINE=2329200; PubMed=8387990;

RN MEDLINE=3259200; PubMed=8387990;

RN SEQUENCE FROM N.A.

SECUENCE OF 225-374 FROM N.A.

SECUENCE OF 225-374 FROM N.A.

SECUENCE FROM N.A.

RN SEQUENCE FROM N.A.

RN SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SECUENCE S. Lesneri; STRAIN=301 / Serctype 2a;

RN MEDLINE=2272406; PubMed=12384590;

RA VIN G. Yang F., Zhao A., Gao Y., Zhao J., Yang G., M.

RA Sun L., Xue Y., Zhao A., Gao Y., Zhao J., Yang G., M.

RA Sun L., Xue Y., Zhao A., Gao Y., Zhao J., Yang G., M.

RA Sun L., Xue Y., Zhao A., Gao Y., Zhao J., Yang G., M.

RA Yul G.

Cheng R. V. Wang Y., Zhao A., Gao Y., Zhao J., RA

Yul G.

RN MEDLINE=22590274; PubMed=127041(2002).

RN SEGUENCE FROM N.A.

RN
                                                                                                                                                                                                                                                                               EMBL; AL049491; CAB39812.1; ALT_INIT.
EMBL; AL583923; CAC30893.1; ALT_INIT.
Leproma; ML1938; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                  (Potential).
-!- SMILARITY: Belongs to the ABC-2 integral membrane protein family.
-!- SIMILARITY: TO E.COLI YBHR AND YBHS AND TO THE C-TERMINAL OF E.COLI YHIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of Shigella ... Ilexara: serotype 2a strain 2457F.", Ilexara: serotype 2a strain 2457F.", Infect. Immun. 71:2775-2786(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L02370; AAC61886.1; -...EMBL; AAC51886.1; -...EMBL; AAC51886.1; -...EMBL; AAC1538, AAN44960.1; ALT_INIT.
EMBL; AAC014592; AAP32.1; -...ECGENE; EG11767; yhhJ.
InterPror; IPRO00412; ABC transpt2.
PROSITE; PSO0890; ABC2 MEMBRANE; 1.
Hypothetical protein; Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 38;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
02895FB13F493391 CRC64;
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U00039; AAB18460.1; ALT INIT.
EMBL; AE000424; AAC76510.1; ALT INIT.
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TRANSMEM 23
TRANSMEM 173
TRANSMEM 230
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TRANSMEM
TRANSMEM
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           RARAR REPRESENTATION OF THE PROPERTY OF THE PR
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074569 operious ci 082167 streptcomyce 088613 pseudomonas 088613 pseudomonas 088613 pseudomonas 08762 xylella fas 08762 xylella fas 08762 xylella fas 08905 cylella fas 08905 cylella fas 08905 cylella fas 08905 calmonalla 08905 calmonalla 08905 salmonalla 0917 osamonalla 0917 osamonalla 0917 osamonalla 0917 canorhabdi 0917 canorhabdi 0917 canorhabdi 0917 canorhabdi 0817 senopus las 0818 sendomonas 08118 pyrococcus 08118 pyrococcus 08118 pyrococcus 08118 pyrococcus

Perfect score:

Sequence:

Searched:

Database

OM protein

Run on:

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SEQUENCE FROM N.A. Curlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T.; Curlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T.; "Prolactin-releasing peptide (PrRP) in the ewe: cDNA cloning, mRNA distribution and effects on prolactin secretion in vitro and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8WN12 PRELIMINARY; PRT; 98 AA.
Q8WN12,
Q8WN12,
Q1-WAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Preproporolactin-releasing peptide.
Ovis aries (Sheep).
Bukaryotas Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinee; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.1%; Score 109; DB 6; Length 9B; 100.0%; Pred. No. 9.7e-09; tive 0; Mismatches 0; Indels
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF450453; AAL4178.1; -.
SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAAB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Q986U6
Q986U6
Q986U6
Q20170
Q7URC6
Q8AJ359
Q8AH95
O50128
Q8U112
Q8U112
Q8U112
                                              0911W4
074569
074569
0886TB7
08FKJ9
09FKJ9
09FKJ9
09FH76
09PH76
09BM86
09BM86
09BW86
09BW80
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(TrEMBLrel. 12, I
(TrEMBLrel. 19, I
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Best Local Similarity 100.0
Matches 19; Conservative
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01-NOV-1999
01-NOV-1999
01-DEC-2001
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45.5
5.5
5.5
Q9W624
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Q9W624
ID Q9W6
AC Q9W6
DT 01-N
DT 01-N
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Q8WN12
   Q8wn12 ovis aries O9w624 carassius a Q72cy1 homo sapien Q6687 homo sapien Q8ww85 homo sapien Q8L168 mus musculu Q8L168 mus musculu Q8L162 agrobacteri Q9664 homo sapien Q81cy2 homo sapien Q81cy2 homo sapien Q81cy2 homo sapien
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027142 methanobact
Q82rv0 streptomyce
076383 caenorhabdi
                                                                                                                                                                                                    August 12, 2004, 14:37:35 ; Search time 27.5581 Seconds (without alignments) 228.984 Million cell updates/sec
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               - protein search, using sw model
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
5: Sp_invertebrate:*
6: Sp_mammal:*
7: Sp_nhage:*
7: Sp_phage:*
7: Sp_phage:*
7: Sp_phage:*
7: Sp_organelle:*
7: Sp_or
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110
1 TPDINPAWYAGRGIRPVGRX 20
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Q9W624
Q9W624
O606871
O606871
Q8WB5
Q8R054
Q8R054
Q8RK052
Q8CKD2
Q8CKD2
Q8CKD2
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Q8CKD2
Q8CKD3
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Maximum DB seq length: 200000000
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Last sequence update) Last annotation update)

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1 TPDINPAWYAGRGIRP 16
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20,
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2 2 3 ,
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Best Local Similarity 56.2
Matches 9; Conservative
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01-0CT-2003 (TrEMBLrel. 2

01-0CT-2003 (TrEMBLrel. 2)

01-0CT-2003 (TrEMBLrel. 2)

Hypothetical protein.

RB6951.

Rhodopirellula baltica.
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les 9, Conservative
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Q7UPG7
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                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
Kurosawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
Rakestraw K.M., Naeve C.W., Look T.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 0.32;
                                                                                                                                                         TIŜSUE=Brain;
Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035608; CAB55682.1; -.
NON_TER 54 54
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
DJ479J7.3. (Sushi-repeat protein (SRPUL)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 AA
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01-AUG-1998 (TrEMBLrel. 07, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                             SPEIDPFWYVGRGVRPIGR 74
                                                                                                                                                                                                                                                                                                                                                                                 1 TPDINPAWYAGRGIRPVGR 19
                     Carassius auratus (Goldfish).
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56.2%;
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18 TPAVTPTWYAGSGYYP 33
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les 9; Conservative
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Best Local Similarity 6
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                                                                                                                                        SEQUENCE FROM N.A.
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amide.
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Matches
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SEQUENCE FROM N.A. Huang C., Chen Y., Huang C.-H., Chen H., Peng J., Chen Y., "Cloning and characterization of the sushi-repeat containing protein (SRP) as a novel interaction partner of Rh type C glycoprotein (RRCG).",
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                Strausberg R.;
Strausberg R.;
Submitteed (JAN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, BC020733; AAH207313.1;
GO; GO:0006118; P:electron transport; IEA.
RILEPPO: IPR001128; Cytochrome_P450.
RILLEPPO: IPR003410; Hyalin.
RILLEPPO: IPR000436; Sushi_SCR_CCP.
RILLEPPO: IPR000436; Sushi_SCR_CCP.
RPEan; PF020494; HYR; 1.
RPEan; PF000044; sushi; 3.
RNART; SMO0032; CCP; 3.
RPROSITE; PS000086; CYTOCHROME_P450; 1.
RPROSITE; PS000086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.8%; Score 57; DB 4; Length 465; 56.2%; Pred. No. 3; 6; Indels ive 1; Mismatches 6; Indels
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Last annotation update)
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Last sequence update)
Last annotation update)
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Q8UKP2;
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                                                                                                             Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                          QBR054 PRELIMINARY; PRT; 467 AA.
QBR054; PRELIMINARY; PRT; 467 AA.
QBR054; Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to sushi-repeat protein.
1110033507RR.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Muscul LaxID-10090;
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Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales,
Planctomycetaccae, Pirellula.
NCBI_TaxID=117;
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.3%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 2; Indels (
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Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO28307, AAH28307.1; --
NGD, MGJ:1916042; 1110039C07Rik.
RGJ, GO:0060118; P:lelectron transport; IEA.
InterPro: IPR001128; Cytochrome_P450.
InterPro: IPR001128; Cytochrome_P450.
InterPro: IPR00413; Sushi,SCR_CCP.
FFam; PF00084; Sushi,SCR_CCP.
FFam; PF00084; Sushi,3.
RPARRI; SN00032, CCP.
RPANRI; SN00032; CCP.
RPANRI; SN00032; CCP.
RPANRI; SN00038; CYTOCHROME_P450; 1.
SEQUENCE 467 AA, 53009 MW; EB4C01C7E6118BE0 CRC64;
                                                                                                                                                                     strain 1.";
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL; BX294145; CAD75095.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 1120 AA; 123221 MW; 67C757B73421BF9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9KIF8 PRELIMINARY, PRT, 468 AA. Q8KIF8; Q8KIF8; Q1-0CT-2002 (TEMBLrel. 22, Created) 01-0CT-2002 (TEMBLrel. 22, Last sequence update) 01-0TN-2003 (TEMBLrel. 24, Last annotation update) Sushi-repeat containing protein.
                                                                                    STRAIN=1;
MEDLINE=22735913; PubMed=12835416;
                                                                                                                                                                                                                                                                                                                                          :|:|||:| ||||
202 EISPAWWAKMGIRP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PDINPAWYAGRGIRP 16
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SEQUENCE FROM N.A.
                                                                    SEQUENCE FROM N.A.
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DEDINE FROM N.A. MEDDREG = 11743193; Monks D.E., Kitajima J.P., Mod D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Nood D.W., Setubal J.C., Kaul R., Mood G.E., Almeida N.F. Jr., Woo L., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo E., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmisti A., Eavy R., Li M.-J., McClelland E., Palmisti A., Raymond C., Rouse G., Saenphimmentak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nester B.W.;
"The genome of the natural genetic engineer Agrobacterium tumefaciens (FRR ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=2160851; Pubmed=11743194; Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Halling C., Mullin D., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Saar C., Strub G., Cielo C., Slater S., "Genome sequence of the plant pathogen and biotechnology agent
                                                                                                                                                                                             [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Huang C.-H., Chen H., Peng J., Chen Y.;
Rioning and characterization of the sushi-repeat containing protein "Cloning and characterization partner of Rh type C glycoprotein (RRP) as a novel interaction partner of Rh type C glycoprotein (RRDG).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
48.2%; Score 53; DB 11; Length 468;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF395640; AAM75691.1; -.
N MOJ, MCI:1916042; 1110039007Rik.
MOJ, GO:006018; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR004410; Hyalin.
InterPro; IPR004436; Sushi_SCR_CCP.
Pfam; PF00084; sushi; 3.
SWART; SM00032; CCP; 3.
PROSITE; PS00086; CYPOTRONE P450; 1.
SEQUENCE 468 AA; 53180 NW; 151A952070D040D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ABC transporter, substrate binding protein.
UGDB OR ATUSO58 OR AGR PAT 77.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PDINPAWYAGRGIRP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 PAVTPTWYAGSGYSP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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OGBUXP2

10 01-47

OGBUXP2

DT 01-47

DT 01-47
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A STRAUSBORG R.;
A STRAUSBORG R.;
Strausborg R.;
Strausborg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL, BC029202; AAH29202.1; -..
R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:0005634; C:nucleus; IEA.
R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
R GO; GO:000548; P:sex differentiation; IEA.
DR Fifat, PF00715; DM DNA-binding.
DR Fain, PF00715; DM DNA-binding.
DR FAIT, SM00301; DM; 1.
DR PROSITE; PS40000; DM DOMAIN.1; 1.
DR PROSITE; PS50809; DM DOMAIN.1; 1.
DR PROSITE; PS50809; DM DOMAIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC032266; AAH32266.1; -
GO, GO:0005634; C:nucleus; IEA.
GO, GO:0003700; F:transcription factor activity; IEA.
GO, GO:0007548; P:realactiption of transcription, DNA-dependent; IEA.
GO; GO:0007548; P:sex differentiation; IEA.
FINEATER: DR DNA-binding.
FEAN: PF00751; DM-domain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
   Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
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PROSITE; PS50809; DM DOWAIN 2; 1.
SEQUENCE 367 AA; 39155 MM; PBB69FF095CAAA28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBIXT2;
01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to RIKEN CDNA 4933432E21 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
46.4%; Score 51; DB 4;
Best Local Similarity 37.5%; Pred. No. 19;
Matches 12; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 4;
Pred. No. 19;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 TPSVPPNPAWISLLHPCGPPAPAGGRGFQPVG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 TPSVPPNPAWISLLHPCGPPAPAGGRGFQPVG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPDI--NPAWYA-----GRGIRPVG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch
1 Similarity 37.5%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
   Eukaryota, Metazoa,
Mammalia, Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE=Testis;
                                                                                                                                                          IISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003
01-MAR-2003
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SEQUENCE
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Q8IXT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
Q8CGW9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
      à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Characterisation of the human DM gene family.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ291699, CAC40652.1;

R EMBL, AJ291699, CAC40652.1;

R Golew, HGNC:1391; DNRTC2.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005635; P:regulation factor activity; IEA.

R GO; GO:0007548; P:sex differentiation; IEA.

R DTGAT; PRO01275; DM DNA-binding.

R InterPro; IPR001275; DM DNA-binding.

R MARR; SM00301; DM; 1.

R PROSITE; PS50609; DM_DOMAIN 1; 1.

M NAM PROSITE; PS50609; DM_DOMAIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                    47.3%; Score 52; DB 16; Length 419; 36.8%; Pred. No. 15; 7; Indels iive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.4%; Score 51; DB 4; Length 333; 37.5%; Pred. No. 17; 37.5%; Ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                         45078 MW; FD99270EFB9F4525 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 AA; 35242 MW; E23F1AA22B8911F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to RIKEN cDNA 4933432E21 gene.
Homo sapiens (Human).
                                                    EMBL, AE008931; AAL45750.1; --
EMBL, AE008931; AAL45750.1; --
PIRBL, AAE0078978, AAK90433.1; --
PIR, AH3166, AH3166.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0006810; F:transporter activity; IEA.
GO; GO:0006810; F:transport; IEA.
InterPro; IPR006059; SBP_bac_1.
Pfam; PF01547; SBP_bac_1.
Plasmid; Complete Protecome.
SEQUENCE 419 AA; 45078 MW; FD99270EFB9P452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 TPSVPPNPAWISLLHPCGPPAPAGGRGFQPVG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPDI -- NPAWYA-----GRGIRPVG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           096524,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequenc
01-UUN-2003 (TrEMBLrel. 24, Last annotate
Doublesex-mab-3 (DM) domain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 SPEANATWFAGTGYLPINK 341
Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TPDINPAWYAGRGIRPVGR 19
                                    Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 36.5.
T; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 37.5
es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ottolenghi C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Q8N6Q2;
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Search completed: August 12, 2004, 14:49:06 Job time: 27.5581 secs
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PIR; B69009;
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STRAND=CB7BL/G07 TISSUE=Testis;
MEDLINE=CB7BL/G07 TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                       Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoong L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietroveki J., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";

EMBL; AE000877; AAB855591; -.
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                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales;
Methanobacteriaceae, Methanothermobacter.
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PROSITE; PS40000; DM DOMAIN_1; 1.
SEQUENCE: PS50809; DM DOMAIN_2; 1.
SEQUENCE 370 AA; 39095 MW; F4DFCB23C94C8A6C CRC64;
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MEDLINE=98037514; PubMed=9371463;
 01-OCT-2003 (TrEMBLrel. 25, Last a Doublesex and mab-3 related transommerc2 OR 4933432E21RIK OR DMRT7.
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                                                                     NCBI_TaxID=10090;
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Sakaki Y., Hattori M., Omura S.;
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Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005021; BAC67752.1; -.
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MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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InterPro; IPR002510; Peptidase_U62.
Pfam: PP01523; PmbA_TldD; 1.
Complete proteone.
SEQUENCE 430 AA; 46062 MW; C4FAE47C111749E6 CRC64;
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MEDLINE=22608306; PubMed=12692562;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Pred. No. 22;
0; Mismatches 4
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SEQUENCE 130 AA;
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August 12, 2004, 14:37:35 ; Search time 42.4419 Seconds (without alignments) 133.146 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 TPDINPAWYAGRGIRPVGRX 20
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6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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ID	AAW31370	AAW95185	ABU60830	AAW31374	AAW95191	AAW97232	AAY49301	AAB10350	AAB90996	AAB46954	AAG62519	AAE26402	ABU60834	~	AAW95192	AAB10351	AAG62520	ABU60835	AAW31376	AAW95193	AAB10352	AAG62521	ABU60836	AAW31371	AAW95188
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### ALIGNMENTS

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888888	sequence in AAW31368. This fragment was obtained by purification and analysis of the N-terminal sequence of a P-2 fraction which is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a centrain nervous system modulator or a pituitary function modulator. This ligand could have specific
ပ္ပ	a pancreatic function modulator. This ligand could have specific

e.g. to treat semile dementia; Alzheimer's, Parkinson's or Huntington's diseases, Creutzfeld-dakease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis, epilepsy and many others, also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of polypeptide by as source of cell lines. The ligand polypeptide as source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisers, in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine pituitary-derived ligand polypeptide obtained by N-terminal sequence analysis

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applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyperpayand polyphagia, hypercholesterolaemia, hyperglyceridaemia, panoreatitis, hyperlipidaemia, hyperprolactinaemia, diabetes, cancer, panoreatitis, hyperlipidaemia, hyperprolactinaemia, diabetes, cancer, panoreatitis, renal disease, Turner's syndrome, neurosis, rheumatoid arthritis, spinal myocardial infarction, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, athma, epilepsy, infertility and/or oligogalaencia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the g protein-coupled receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; PSRN10; UNF1.1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creuzzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.
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Pred. No. 2e-10;
0; Mismatches 0; Indels
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Matches 19; Conserv
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Length 19; 0; Indels

Score 109; DB 2; Pred. No. 2e-10;

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Ouery Match Best Local Similarity 100.8 Matches 19, Conservative

Sequence 19 AA;

1 TPDINPAWYAGRGIRPVGR 19

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1 TPDINPAWYAGRGIRPVGR

Mismatches

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The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides generacing protein applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
                                                                                                    Peptide production by gene recombination associated peptide #14.
                                                                                                                             Peptide production; low-molecular peptide; KiSS-1; GPR8 ligand; gene recombination.
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                                                                                                                                                                                                                                                                                                                                                                                               Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 60; 87pp; Japanese.
ABU60830 standard; peptide; 19 AA.
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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPRIO (human) or URR-I (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate ligand polypeptide of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically,

New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening.

Fukusumi S;

Hinuma S,

WPI; 1999-009423/01

Example 16; Page 145; 206pp; English.

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Gaps

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Indels

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Mismatches

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19; Conservative

g ò

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 34 to 53 of the sequence in AAW13168 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This containing this ligand may be used as a pituitary function modulator. This cannot also be specific applications as a prophylactic or therapeutic agent for dementa, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyperinpidaemia, amylotrophic lateral sclerosis, acute myocardial infarction, spinocerbellar degeneration, bone fracture, trauma, atopic dermatitis, osteoprosis, asthma, epilepsy, infertility and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein
                              ö
                                                                                                                                                                                                                              protein-coupled receptor; ligand binding; pharmaceutical; modulator; ltuitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fukusumi S;
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0
                                                                                                                                                                                                         Bovine G protein-coupled receptor ligand peptide fragment 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 109; DB 2; Length 20;
Pred. No. 2.1e-10;
         19;
                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujii R,
         Length
         DB 6;
2e-10;
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                                 Mismatches
         Score 109;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Habata Y, Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 161; 258pp; English.
99.1%; Scc.
100.0%; Pre
                                                                                                                                     AAW31374 standard; peptide; 20 AA.
                                                                     1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.1%; (
100.0%;
                                                                                                                                                                                                                                                                                                                                                                      95JP-00343371.
96JP-00059419.
96JP-00211805.
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                                                                                                                                                                                 (first entry)
    99.1.
Best Local Similarity 100.1
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-363672/33.
N-PSDB; AAV02397.
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Best Local Similarity
                                                                                                                                                                                                                                                        therapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                      28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
18-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                 26-DEC-1996;
                                                                                                                                                                                   06-APR-1998
                                                                                                                                                                                                                                                                                                                          10-JUL-1997.
                                                                                                                                                                                                                                                                             Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinuma S,
Kitada C;
                                                                                                                                                            AAW31374;
                                                                                                                       AAW31374
ID AAW3
                                                                                                             RESULT 4
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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated CRR10 (human) or UHR-11 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant to the ligand polypeptide encoding DNA are used to produce a recombinant contains the ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the piulitary, central nervous system, pancreas and other contains and the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, control real semile dementia; Alzheimer's, Parkinson's or Huntington's disabetes; schizophrenia; disorders of growth hormone secretion; cancer; rehungation entritional status and ass vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to carrying the ligand polypeptide encoding DNA or its mutein animals contains of the polypeptide expressing genes, as models of disabet, for drug screening and as source of cell lines. The ligand contains a source of probes and primers; to identify contains and assource of cell lines. The ligand antisera; in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine genome-derived ligand commimals. The present sequence represents a bovine genome-derived ligand contains a similar to the murine ligand-polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapettic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; polosoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sovine pituitary-derived ligand polypeptide fragment.
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13
                                                                      TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                      AAW95191 standard; peptide; 20
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1 TPDINPAWYAGRGIRPVGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9849295-A1
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                                                                                                                                                                                                                RESULT 5
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Length 20;

DB 2;

Score 109;

99.1%;

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Page

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Gaps

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Indels

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Mismatches

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19; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine pituitary-derived ligand, modulation, prolactin secretion, G protein-coupled receptor, GPCR, hypoovarianism, gonecyst cacogenesis, menopausal syndrome; euthyroid, hypometabolism, lactation, pituitary adenomatosis, brain tumour, emmeniopathy; autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a bovine pituitary-derived ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolatin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolatin secretion can be used for treating or preventing prolatins generating expensis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic manmal and as an aphrodisiac. The agents for inhibiting prolatin secretion can be used for treating or preventing publicating and agents for inhibiting prolatin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prolactinoma, infertility; impotence; amenorrhea; galactorrhea; acromegaly, Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Frobes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy.
                                                                      Gaps
                                                                  .,
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine pituitary-derived ligand polypeptide fragment.
                        Pred. No. 2.1e-10; Mismatches 0;
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100.001; tr
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                                                                                                                           TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                      TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                        AAW97232 standard; peptide; 20
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                                                               Conservative
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                        Similarity
19; Conserv
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                        Best Local
Matches 1
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                                                                                                                                                                                                                                                                                                RESULT 6
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Monoclonal antibody, 19P2 ligand, diagnosis, prolactin secretion, pituitary, regulatory mechanism, central nervous system, pancreatic.

19P2 ligand peptide fragment

(first entry)

22-FEB-2000

AAY49301 standard; peptide; 20 AA.

RESULT 7

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/note= "C-terminal amide" Location/Qualifiers

Key Modified-site

30s sp.

WO9960112-A1

25-NOV-1999,

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Hinuma

Kitada C,

Matsumoto H,

98JP-00140293. 99WO-JP002650

20-MAY-1999; 21-MAY-1998; (TAKE ) TAKEDA CHEM IND LTD.

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                                                                                                                                                                                                                                                                                                                                                                                      New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand
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100.0%; Pred. No. 2.1e-10;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 27; 73pp; Japanese.
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Matches
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AAB10350
ID AAB1:
XX
AC AAB1:
XX
DT 24-N
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24-NOV-2000 (first entry)

Score 109; DB 2; Length 20; Pred. No. 2.1e-10;

99.1%; S 100.0%;

Query Match Best Local Similarity Sequence 20 AA;

prolated; descriptions, constructions, constructions, constructions, infertility, impotence, amenorrhea, galactorhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Forbes-hibbitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia

99US-0134406P. 99US-0153406P. 99US-0159783P.

17-MAY-1999; 10-SEP-1999; 15-OCT-1999;

(CONJ-) CONJUCHEM INC.

17-MAY-2000; 2000WO-US013576.

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This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion
                                     Bovine; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                              Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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           Bovine oxytocin secretion promoting peptide SEQ ID NO:
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100.0%; Pred. No. 2.1e-10;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 51; 72pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TPDINPAWYAGRGIRPVGR 19
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
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comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a copelidase stabilised therapeutic peptides composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth cathorise and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent composition due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half intracellular uptake and interference with physiological processes. AABS0829 to AABS0441 represent invention

Examplification of the present invention
                                                                                                                                                                            Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPRIO; UHR-1; PrRP receptor; prolactin-releasing peptide; pain; central nervous system disorder; autonomic regulation; analgesic; hypotensive; blood pressure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                        invention describes a modified therapeutic peptide
                                                                                                                   Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 109; DB 4; I
Pred. No. 2.18-10;
                                                                                                                   Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "C-terminal amide"
                                                                                                                                                                                                                           Disclosure; Page 245; 733pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.1%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB46954 standard; protein; 20 AA
                                                                                                                     Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYAGRGIRPVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide PrRP20 fragment.
                                                                                                                      Ezrin AM,
                                                                                                                                                  WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200109182-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-2001.
                                                                                                                      Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB46954;
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This invention describes a novel C-terminal fragment (I) of an isolated CC prolactin-releasing peptide (PrRP), referred to as PrRP20 and having a sequence (SI). The invention also describes (I) a therapeutic composition (CI) comprising (I) or a C-terminal fragment of PrRP referred to as PrRPB and comprising (I) or a C-terminal fragment of PrRP referred to as PrRPB and comprising (SI); (2) a diagnostic method based on antisera against PPRPSO for identification of disorders involving the central C regulation, where specific antisera against the N-and/or C-terminal control or autonomic credulation, where specific antisera against the N-and/or C-terminal cevels; (3) a rat or human receptor encoded by a 1122 nucleotide sequence (S3), fully defined in the specification; (4) treating a person suffering from a disorder regulated by a receptor (II) encoded by a sequence of the receptor; and (5) treating blood pressure, by blocking of receptors the receptor; and (5) treating blood pressure, by blocking of receptors of PRPP or its C-terminal fragment GlyllahrgprovalGlypargher activity.

(I) is useful for regulating autonomic functions, such as increasing blood pressure. (I) is useful for treating pain, for mendicament for regulating blood pressure, and for treating pain. Agonist conductance the requiating blood pressure.

CC and antagonist of (II) are useful for treating autonomic functions and treating high hood pressure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.
                                                                                                                                                   C-terminal fragments of prolactin-releasing peptide useful for regulating autonomic functions and in the manufacture of a medicament for regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cow; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.1%; Score 109; DB 4; Length 20; 100.0%; Pred. No. 2.1e-10; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine CRH releasing protein related peptide SEQ ID NO: 6.
                                                                              Korpi
                                                                              ΕŪ
                                                                            Kalso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG62519 standard; peptide; 20 AA.
                                                                                                                                                                                                                              Claim 1; Page 10; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYAGRGIRPVGR 19
                                      (JUVA-) JUVANTIA PHARMA LID OY
  20-MAR-2000; 2000US-00531567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuropathic pain, for high blood pressure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000; 2000WO-JP008119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-1999; 99JP-00327900.
26-SEP-2000; 2000JP-00297073.
                                                                            Pertovaara A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
es 19; Conservative
                                                                                                                 WPI; 2001-182941/18.
                                                                                                                                                                                          blood pressure.
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Use of G protein receptor ligand or peptide for controlling corticotropin
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                                                                                                                                                                                  The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adreanal gland hypofunction and obesity. The incentic sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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99.1%; Score 109; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine PrRP-31 C-terminal peptide, PrRP-20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE26402 standard; peptide; 20 AA.
                                                                                                                                                       Claim 4; Page 64; 90pp; Japanese.
                                             Matsumoto H, Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPDINPAWYAGRGIRPVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-2001; 2001US-00932161.
                                                                                                                           releasing hormone secretion.
             (TAKE ) TAKEDA CHEM IND LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-2000; 2000US-00560915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                           WPI; 2001-355552/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CIVE/) CIVELLI O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002037533-A1.
                                                                                                                                                                                                                                                                                                                                                              Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-2002
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                                             Kitada C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              civelli o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apnea, compantagonist.
                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE26402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
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Disclosure; Page 24; 35pp; English

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The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PRRP) receptor (GPR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. The receptor agonists may be used to treat common disorders which lead to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and for treatening insomnia such as adjustment sleep disorder and psychophysiologic insomnia. The present sequence is bovine PRRP-31 C-terminal peptide, PRRP-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by lightion in a precursor protein. The method is for producing (low-molecular) peptide e.g. KiSS-1 peptide and GRRB lighnd for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide production by gene recombination associated peptide #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide production; low-molecular peptide; KiSS-1; GPR8 ligand; gene recombination.
                                                                                                                                                                                                                                                                                                                                          99.1%; Score 109; DB 5; Length 20; 100.0%; Pred. No. 2.1e-10; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU60834 standard; peptide; 20
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                          Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU60834
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20 AA

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Gaps

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This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 34 to 54 of the sequence in AMN1368 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This city of man are assay to modulator. This containing this ligand may be used as a prophylactic or therapeutic capent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone consciousness, mayer and polyphagia, hypercholesterolaemia, chyperglyceridaemia, hyperlipidaemia, hyperglyclocinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, amylotrophic lateral scherosis, armsient brain ischaemia, appincerbellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein
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                                                                                                                                                                                                                                                                                                                                  protein-coupled receptor; ligand binding; pharmaceutical; modulator;
Liuitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland
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 Length 20;
                                 Indels
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Kitada C;
99.1%; Score 109; DB 6; I 100.0%; Pred. No. 2.1e-10; ive 0; Mismatches 0;
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                                                                     1 TPDINPAWYAGRGIRPVGR 19
                                                                                                    1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                              AAW31375 standard; peptide; 21
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96JP-00059419.
96JP-00211805.
96JP-00246573.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-JP003821,
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-363672/33.
                      Similarity
                                                                                                                                                                                                                                                                                                                                                         pituitary; centratherapeutic agent.
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12-AUG-1996;
18-SEP-1996;
 Query Match
Best Local Simil
Matches 19; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus.
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                                                                                                                                                              RESULT 14
AAW31375
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   Indels
                                                  Bovine pituitary-derived ligand polypeptide fragment
                               AAW95192 standard; peptide; 21 AA
         1 TPDINPAWYAGRGIRPVGR 19
            1 TPDINPAWYAGRGIRPVGR 19
                                            (first entry)
   Conservative
Best Local Similarity
Matches 19; Conserv
                                            10-MAR-1999
                                      AAW95192;
                            AAW95192
                               Сp
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Pitultary-derived ligand polypeptide; G-protein coupled orphan receptor; PSRRIO; UNF-1; modulator; pitultary; central nervous system; pancreas; tissue; screen; therapeutic; pitultary; central nervous system; pancreas; Alzheimer's disease; Parkinson's disease; Huntington's disease; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Centrzfeld-dakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.

WO9849295-A1

27-APR-1998;

28-APR-1997;

Hinuma S,

for drug screening. treating

The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated CPRIO (human) or URR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other contains and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a colypeptide to the receptor; to quantify the amount of receptor in a colypeptide to the receptor; to quantify the amount of receptor in a colypeptide to the receptor; to quantify the amount of receptor in a colypeptide and to raise antibodies. They may also be used therapeutically, colypeptide and to raise antibodies. They may also be used therapeutically, colypeptide arthritis, epilepsy and many others, also to improve post. The newmatoid arthritis, epilepsy and many others, also to improve post. The mention of the polypeptide encoding DNA or its mutein are used to struck the function of the polypeptide encoding DNA or its mutein are used to struck the function of the polypeptide encoding DNA or its mutein are used to disease, for drug screening and as source of cell lines. The ligand polypeptide as source of cell lines, for indensity or related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine genome-derived ligand company and a similar to the murine ligand-polypeptide

Sequence 21 AA,

ö polypeptide ligand for orphan G protein coupled receptors - used for ating disorders of central nervous system, pituitary and pancreas, and Gaps Pred. No. 2.2e-10; Mismatches 0; 100.0%; Prea. .... Example 19; Page 151; 206pp; English. 97JP-00109974. 98WO-JP001923, (TAKE ) TAKEDA CHEM IND LTD Fukusumi S; WPI; 1999-009423/01 JS-NOV-1998. Bos sp.

ö Gaps ö Length 21; 0; Indels Score 109; DB 2; I Pred. No. 2.2e-10; 0; Mismatches 0; 99.1%; Scor 100.0%; Pre Query Match
Best Local Similarity 100.
Matches 19, Conservative

1 TPDINPAWYAGRGIRPVGR 19 TPDINPAWYAGRGIRPVGR 19

셤 8

completed: August 12, 2004, 14:43:55 ne : 42.5669 secs Search cor Job time

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August 12, 2004, 14:49:10 ; Search time 35.3488 Seconds (without alignments) 177.617 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                              1292805
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                1292805 seqs, 313927144 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
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1 TPDINPAWYAGRGIRPVGRX 20
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                       Searched:
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## Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Published Applications AA:* 1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:* 2: /cgn2_6/ptodata/2/pubpaa/PCT NEW FUB.pep:* 3: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:* 4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:* 5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:* 6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:* 7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:* 8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:* 9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:* 11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:* 11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:* 12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:* 13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:* 14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:* 15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:* 16: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:* 17: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:* 18: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:* 17: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:* 18: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:* 18: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

	Description	Sequence 27, Appl	Sequence 16, Appl	Sequence 42, Appl	_	Sequence 43, Appl	Sequence 44, Appl	Sequence 13, Appl	Sequence 39, Appl	Sequence 13, Appl	Sequence 40, Appl	_		Sequence 38, Appl	Sequence 82, Appl	Sequence 84, Appl
SUMMARIES	ΩI	US-10-044-592-27	US-09-932-161-16	US-10-044-592-42	US-10-096-777-16	US-10-044-592-43	US-10-044-592-44	US-09-932-161-13	US-10-044-592-39	US-10-096-777-13	US-10-044-592-40	US-10-044-592-41	US-10-044-592-28	US-10-044-592-38	US-10-044-592-82	US-10-044-592-84
	DB	13	σ	13	14	13	13	σ	13	14	13	13	13	13	13	13
	% Query Match Length DB	19	20	20	20	21	22	31	31	31	32	33	96	98	96	98
	% Query Match	99.1	99.1	99.1	99.1	99.1	1.66	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1	99.1
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4-592-8	0-044-5	09-932-161-1	0-044-5	-10-09	US-09-932-161-14	5-10-04	US-10-044-592-5	10	-10 - 04	-10-044-59	-044-5	-10-044-5	10-044-592-	US-09-932-161-18	3-10-096-777-	39-932-16	0-096-777-	-10	0-044-59	0-044-	-10-301-822-1	-424-599-26	738-626-464	US-10-156-761-75	US-10-369-493-6	US-10-389-647-46	US-10-044-592-9	US-10-156-761-10748	US-10-424-599-151465
13	13	6	133	14	σ	13	13	14	13	13	13	13	13	6	14	σ	14	13	13	13	14	12	σ	14	15	12	13	14	12
86	ω ω	20	50	70	31	31	31	31	70	82	86	91	29	20	20	31	31	87	25	9	465	183	•	m	527	9	10	402	140
99.1	99.1	95.5	95.5	95.5	95.5	95.5	95.5	'n	'n	'n.	'n.	95.5	4.	m.	ص	ω.	ω.	ω,	85.5	Ξ.	Η.	~	47.3	S	'n		43,6		42.7
109	109	105	105	105	105	105	105	105	105	105	105	105	104	103	103	103	103	103	94	57	57	52	52	50	50	48.5	48	48	47
16	17	80	13	20	21	22	23	24	25	26	27	28	29	0	31	32	33	3.4	មា	36	3.7	80	66	4 4	41	4.2	43	44	45

### ALIGNMENTS

Database :

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Gaps
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0
US-10-044-592-2/

Sequence 27, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinma, Shuji

APPLICANT: Hinma, Shuji

APPLICANT: Hinma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use

FILE REFERENCE: 2463US2B

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: US 99/403639

PRIOR FILING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR FILING DATE: 1999-25-10

PRIOR FILING DATE: 1999-04-28

NUMBER: OF EQ ID NOS: 96

SOFTWARE:

SEQ ID NO 27

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
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100.0%; Pred. No. 1.8e-09;
live 0; Mismatches 0;
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Best Local Similarity
Matches 19; Conserv
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US-10-044-592-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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RESULT 2 US-09-302-161-16 Sequence 16, Application US/09932161 ; Patent No. US20020037533A1 1 TPDINPAWYAGRGIRPVGR 19 g

1 TPDINPAWYAGRGIRPVGR 19

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Query Match 99.1%; Score 109; DB 14; Best Local Similarity 100.0%; Pred. No. 1.9e-09; Matches 19; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US/09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENTH: 20
TYPE: PRT
ORGANISM: Bos taurus
US-10-096-777-16
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Sequence 44, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
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ORGANISM: Bovine
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LENGTH: 21
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US-10-096-777-16

Sequence 16, Application US/10096777

Publication No. US20030171270A1

SEQUENCE 11

APPLICANT: Civelli, Olivier

APPLICANT: Lin, Steven

TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)

FILE REPRENCE: P-UC 3534

CURRENT APPLICANTE: 2002-03-12
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| Sequence 42, Application US/10044592
| Publication No. US20020143152A1
| GENERAL INFORMATION:
| APPLICANT: Hinuma, Shuji
| APPLICANT: Hinuma, Shuji
| APPLICANT: Fukusumi, Shoji
| TITLE OF INVENTION: PolyPeptides, their Production and Use FILE REFERENCE: 24631922
| CURRENT APPLICATION NUMBER: US/10/044,592
| CURRENT FILING DATE: 1999-25-10
| PRIOR APPLICATION NUMBER: PCT/JP98/01923
| PRIOR FILING DATE: 1999-25-10
| PRIOR FILING DATE: 1998-04-27
| PRIOR APPLICATION NUMBER: UP 9-109974
| PRIOR APPLICATION NUMBER: UP 9-109974
| NUMBER OF SEQ ID NOS: 96
         APPLICANT: Civalia, Olivier
APPLICANT: Civalia, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REPREMENCE: P-UG 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT PILING DATE: 2001-08-17
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4:0
SEQ ID NO 16
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.1%; Score 109; DB 9; Length 20; Best Local Similarity 100.0%; Pred. No. 1.9e-09; Matches 19; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                  TYPE: PRT CORGANISM: Bos.taurus US-09-932-161-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-044-592-42
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LENGTH: 20
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RESULT 5.
US-10-044-592-43

1/Sequence 43, Application US/10044592

| Sequence 43, Application US/10044592
| Publication No. US20020143152A1
| Publication No. US20020143152A1
| GENERAL INPOMATION:
| APPLICANT: Hinuma, Shuji
| TITLE OF INVANITON: Polypeptides, their Production and Use FILE REPRENCE: 2461US2P
| CURRENT APPLICATION NUMBER: US/10/044,592
| CURRENT FILING DATE: 1999-25-10
| PRIOR PILING DATE: 1999-25-10
| PRIOR FILING DATE: 1999-25-10
| PRIOR FILING DATE: 1998-04-27
| PRIOR PILING DATE: 1998-04-27
| PRIOR FILING DATE: 1998-04-27
| PRIOR PILING DATE: 1998-04-27
| PRIOR FILING DATE: 1998-04-27
| PRIOR FILING DATE: 1998-04-28
| NUMBER OF SEQ ID NOS: 96
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APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: PolyPeptides, their Production and Use;
FILE REPERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: US 09/403639
PRIOR PILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR PILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR PILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: UP 9-109974
PRIOR PILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.1%; Score 109; DB 13; Length 21; 100.0%; Pred. No. 2e-09; ive 0; Mismatches 0; Indels
Indels
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US-100.96-777-13

Sequence 13, Application US/10096777

Publication No. US20030171270A1

Sequence 13, INPORMATION:

Publication No. US20030171270A1

GENERAL INPORMATION:

APPLICANT: Lin, Steven

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PTRP)

FILE REFERENCE: P-UC 3534

CURRENT PILING DATE: 200-33-12

PRIOR APPLICATION NUMBER: US/09/560,915

PRIOR FILING DATE: 200-00-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastERQ for Windows Version 4.0

SEQ ID NO: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-10-044-592-40
Sequence 40, Application US/10044592
Sequence 40, Application US/10044592
Publication No. US20020143152A1
GENERAL INPORMATION:
APPLICANT: Hunma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463U526
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-26-10
PRIOR FILING DATE: 1998-04-27
PRIOR RELICATION NUMBER: US/10/JP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR RELICATION NUMBER: US/10/JP98/01923
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR PELICATION NUMBER: US/10/JP9974
PRIOR PELICATION NUMBER: US/10/JP9974
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99.1%; Score 109; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.1e-09;
tive 0; Mismatches 0;
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                       1 TPDINPAWYAGRGIRPVGR 19
                                                                TPDINPAWYAGRGIRPVGR 30
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Bos taurus
US-10-096-777-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Bovine US-10-044-592-40
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US-10-044-592-41
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SEQ ID NO 40
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Sequence 39, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

TITLE OF INVENTION: Polypetides, their Production and Use

FILE REFERENCE: 263US2P

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR PILING DATE: 1999-25-10

PRIOR PILING DATE: 1999-25-10

PRIOR PILING DATE: 1999-25-10

PRIOR PILING DATE: 1997-04-28

NUMBER: OF SEQ ID NOS: 96

SOFTWARE:

SEQ ID NO 39

LENGTH: 31

TYPE: PRI

CREANIEM: BOVINE

US-10-044-592-39
                                                                                                                                                                                                                                                                                                                                          US-09-32-161-13

(Sequence 13, Application US/09932161
) Patent No. US20020037533A1
) GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Seeven
TITLE OF INVENTION: Promoting wakefulness and Sleep
TITLE OF INVENTION: Promoting wakefulness and Sleep
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REPERENCE: P-UC 4679
CURRENT FILING DATE: 2001-08-17
CURRENT FILING DATE: 2001-08-17
PRIOR PILING DATE: 2000-04-28
NUMBER: OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.1%; Score 109; DB 13; Length 31; Best Local Similarity 100.0%; Pred. No. 3e-09; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                        Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

99.1%; Score 109; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                         Indels
                                                                                                                     Query Match
99.1%; Score 109; DB 13;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPDINPAWYAGRGIRPVGR 19
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                                                                                                                                                                                                                       1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bos taurus
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-932-161-13
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Gaps

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Sequence 82, Application US/10044592
Fublication No. US2020143152A1
GENERAL INFORMATION:
TOTALE INFORMATION:
TITLE OF INVENTION: Polypeptides, their Production and Use FILE REFERENCE: 2463182P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR PELING DATE: 1999-25-10
PRIOR PELING DATE: 1998-04-27
PRIOR PILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: DF 9-109974
PRIOR PILING DATE: 1998-04-28
NUMBER OF SEQ ID NOS: 96
       TITLE OF INVENTION: Polypeptides, their Production and Use FILES REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR PILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 38
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 98;
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Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: FURBEBUMI, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT SPLIATON NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
                                                                                                                                                                                                                                                                                                                                                                                                                                       99.1%; Score 109; DB 13; 100.0%; Pred. No. 9.3e-09;
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99.1%; Score 109; DB 13;
Best Local Similarity 100.0%; Pred. No. 9.3e-09;
Matches 19; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Bovine
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                                                                                                                                                                                                                                                                                                                                                                                          US-10-044-592-38
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LENGIH: 98
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Sequence 41, Application US/10044592
Publication No. US20020143152A1
GENERAL INCORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR PLING DATE: 1998-04-27
PRIOR PLING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: UP 9-109974
PRIOR PILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 41
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/10044592
| Publication No. US20020143152A1
| Sequence 28, Application US/10044592
| Publication No. US20020143152A1
| APPLICANT: Hinuma, Shuji
| APPLICANT: Hinuma, Shuji
| TITLE OF INVENTION: Polypeptides, their Production and Use
| PILE REFERENCE: 2463US2P
| CURRENT APPLICATION NUMBER: US/10/044,592
| CURRENT FILING DATE: 2002-01-10
| PRIOR FILING DATE: 1998-05-10
| PRIOR FILING DATE: 1998-04-27
| PRIOR FILING DATE: 1998-04-27
| PRIOR FILING DATE: 1998-04-27
| PRIOR FILING DATE: 1997-04-28
| WUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 99.1%; Score 109; DB 13; Similarity 100.0%; Pred. No. 3.2e-09; 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
99.1%; Score 109; DB 13;
Best Local Similarity 100.0%; Pred. No. 9.3e-09;
Matches 19; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 TPDINPAWYAGRGIRPVGR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYAGRGIRPVGR 19
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APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 19; Consery
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-10-044-592-28
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SOFTWARE:
SEQ ID NO 28
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Sequence 44, Appl Sequence 122, App Sequence 131, App Sequence 136, Appl Sequence 40, Appl Sequence 41, Appl Sequence 51, Appl Sequence 51, Appl Sequence 52, Appl Sequence 52, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 47, Appl Sequence 47

Sequence 131, Sequence 136, Sequence 136, Sequence 50, Sequence 17, Sequence 17, Sequence 51, Sequence 41, Sequence 52, Sequence 52, Sequence 52,

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Query Match

99.1%; Score 109; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.8e-11;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-105-678A-30
; Sequence 30, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER TEACHBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIM FC Compatible
COMPUTER: ISM FC Compatible
COMPUTER: BIM FC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COM11n, David G:
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELEFRONCHION INFORMATION:
TELEFRONCE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, 130 Water Street
         US-08-776-971-44
US-08-776-971-112
US-08-776-971-131
US-09-105-6788-40
US-09-105-6788-40
US-09-421-208-40
US-09-421-208-40
US-09-421-208-40
US-09-60-915-17
US-09-60-915-17
US-09-105-6788-41
US-09-105-6788-41
US-09-105-6788-41
US-09-105-6788-42
US-09-105-6788-42
US-09-105-6788-42
US-09-105-6788-42
US-09-105-6788-42
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US-09-105-6788-42
US-09-105-6788-42
                                                                                                                                                                                                                                                                                               ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide US-09-105-678A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
COUNTRY: UE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02109
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Sequence 30, Appl
Sequence 34, Appl
Sequence 8, Appli
Sequence 99, Appli
Sequence 34, Appli
Sequence 16, Appl
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Appl
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Appli
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                                                                                                     August 12, 2004, 14:37:36; Search time 11.3953 Seconds (without alignments) 90.609 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, 2 Sequence 16, 2 Sequence 35, 2 Sequence 35, 2 Sequence 35, 2 Sequence 36, 3 Sequence 10, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, A
Sequence 97,
Sequence 7,
Sequence 31,
Sequence 32,
Sequence 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36,
Sequence 7, A
Sequence 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32,
Sequence 33,
Sequence 7, A
Sequence 33,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-105-678A-30
US-08-776-971-4
US-09-105-678A-34
US-09-105-678A-34
US-09-105-678A-34
US-09-105-678A-35
US-09-105-678A-35
US-09-105-678A-35
US-09-105-678A-35
US-09-105-678A-35
US-09-105-678A-35
US-09-105-678A-31
                                                                                                                                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                       389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                110
1 TPDINPAWYAGRGIRPVGRX 20
                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                   US-09-700-643A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                     Fotal number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                     Title:
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Gaps

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US-09-421-208-30

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Sequence 4, Application US/08776971B
Sequence 4, Application US/08776971B
Patent No. 622894
GENERAL INFORMATION
Habata, Yugo
Kawamata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
ITILE OF INVENTION POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTE: NAS

CONTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDDIUM TYPE: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

SOFTWARE: FastSEQ for Windows Version 2.0

CLASSIFICATION NUMBER: US/08/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION NUMBER: PCT/JP96/03821

FILING DATE: 28-DEC-1996

APPLICATION NUMBER: UP 7/34371

FILING DATE: 12-MAR-1996

APPLICATION NUMBER: UP 8/291805

FILING DATE: 12-MAR-1996

APPLICATION NUMBER: UP 8/211805

FILING DATE: 12-MAR-1996

APPLICATION NUMBER: UP 8/246573

FILING DATE: 12-MAR-1996

APPLICATION NUMBER: UP 8/246573

FILING DATE: 12-MAR-1996

APPLICATION NUMBER: UP 8/246573

FILING DATE: 12-MG-1996

APPLICATION NUMBER: UP 8/246573

FILING DATE: 12-MG-1996

APPLICATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

TELEPROMENS: G17-523-46440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
99.1%; Score 109; DB 3; I
Best Local Similarity 100.0%; Pred. No. 6.8e-11;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: procein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-776-971-4
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                  US-08-776-971-4
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Gaps
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0
           Length 19;
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Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
99.1%; Score 109; DB 3; I
Best Local Similarity 100.0%; Pred. No. 6.8e-11;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                            PRICH APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
Sequence 30, Application US/09421208 Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYAGRGIRPVGR 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-105-678A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-421-208-30
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COUNTRY:
ZIP: 021
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HOSONA, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: BOSCON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER: EMADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: IBM compatible
SOFTWARE: FastSEQ for Windows Version 2.0
CUBREATING SYSTEM: DOS
CUBREATING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
APPLICATION NUMBER: DCT/JP96/03821
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 18-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

99.1%; Score 109; DB 3; 1

Best Local Similarity 100.0%; Pred. No. 7.2e-11;

Matches 19; Conservative 0; Mismatches 0;
                    PILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONILIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECHMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: JP 8/211805
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 98, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-776-971-98
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Kawanata, Yuji
Hosoya, Masaki
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERIS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

99.1%; Score 109; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.2e-11;

Matches 19; Conservative 0; Mismatches 0; Indels
                       COMPUTER KEADABLE FORM:

MEDIUM TYEE: FIDAPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATORNEY AGENT INFORMATION:
FILING DATE: 27-JUN-1997
ATORNEY AGENT INFORMATION:
FILING DATE: 23-3400
TELEFRAMION TON TONERATION:
TELEFRAMION FOR SEQ ID NO: 34:
SEQUENCE CHARACTER STICS:
LYPE: AMINO acids
TYPE: ATORNEY STANDENDESS:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM compatible
COMPUTER: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastBRO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: _<Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08776971B
Patent No. 622894
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-105-678A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-776-971-8
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0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ELEM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/105,678A
FILING BAPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
RIDING DATE: 2-JUN-1998
RIOR APPLICATION NUMBER: JP 172118/1997
RIDING DATE: 2-JUN-1997
ATTORNEY/AGENT INFORMATION:
           0; Mismatches
                                                  1 TPDINPAWYAGRGIRPVGR 19
                                                                                          1 TPDINPAWYAGRGIRPVGR 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
         19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Bos taurus
US-09-560-915-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 19; Conserv
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ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-105-678A-35
                                                                                                                                                             RESULT 8
US-09-560-915-16
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         Matches
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99.1%; Score 109; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e-11;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.1%; Score 109; DB 3; Length 20; 100.0%; Pred. No. 7.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suchaga, Masato
APPLICANT: Moniya, Takeo
APPLICANT: Moniya, Takeo
APPLICANT: Moniya, Toko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOWKUNICATION INFORMATION:
                                                                                                                                                                                                                                              TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 98:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-7UN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-7UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48466-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/09421208
Patent No. 6258561
                                                                                     TELEPHONE: 617-523-3400
TELEFAX: 617-523-640
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-421-208-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDALL
STREET: 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                   US-08-776-971-98
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Fatent No. 6383764
Fatent No. 638376
Fatent NaPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/09/560,915
CURRENT FILING DATE: 200-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
ENGTH: 20
Gaps
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0
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Patent No. 6103862

GENERAL INFORMATION:
APPLICANT: Buenaga, Masato
APPLICANT: Anoriya, Takeo
INFORMATION: APPLICANT: Anoriya, Yoko
INFORMATION: METHOD OF PRODUCING A 19P2 LIGAND
ITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
CORRESPONDENCE ADDRESS:
ADDRESSEB: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 35:
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Gaps
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                                                                                                       Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Naishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: BOSTON
CITY: BOSTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                       Query Match
99.1%; Score 109; DB 3; Length 21
Best Local Similarity 100.0%; Pred. No. 7.6e-11;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PETENTIN Release #1.0, Version #1.30
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
PILING DATE: 27-JUN-1997
FILING DATE: 27-JUN-1997
FILIN
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99.1%; Score 109; DB 3; L
Best Local Similarity 100.0%; Pred. No. 7.6e-11;
Matches 19; Conservative 0; Mismatches 0;
; SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-08-776-971-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-105-678A-36
; Sequence 36, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-421-208-35; Sequence 35, Application US/09421208; Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TPDINPAWYAGRGIRPVGR 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                   Best Loca
Matches
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Kawamata, Yuji
Habata, Yugo
Kawamata, Yuji
Habata, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
Title Of Invention PolyProteins, Their Production and USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                    Query Match

99.1%; Score 109; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-11;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FASEBOG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION NUMBER: DFT/AP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 9/34371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/21605
APPLICATION NUMBER: JP 8/21605
APPLICATION NUMBER: JP 8/21605
APPLICATION NUMBER: JP 8/26573
FILING DATE: 18-SEP-196
APPLICATION NUMBER: JP 8/26573
FILING DATE: 18-SEP-196
APPLICATION NUMBER: JP 8/26573
FILING DATE: 18-SEP-196
ATTORNEY/AGENT INFORMATION:
NAME: CONINI, DRAY'S G.
REFERENCE/DOCKET NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAK: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08776971B
Patent No. 622894
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYAGRGIRPVGR 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein FRAGMENT TYPE: internal
                         SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                  TYPE: anino acid
STRANDEDNESS:
TOPCLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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US-08-776-971-9
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OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-776-971-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-421-208-36
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NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Toko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                            ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
STTY: Boston
                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-UTN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.1%; Score 109; DB 3; Best Local Similarity 100.0%; Pred. No. 8e-11; Matches 19; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFRENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TPDINPAWYAGRGIRPVGR 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                   STATE: M. COUNTRY:
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US-08-776-971-10
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Gaps
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Patent No. 625851
GENERAL INFORMATION:
APPLICANT: Anenga, Masato
APPLICANT: Analay, Takeo
APPLICANT: Analay, Yakeo
APPLICANT: Analay, Yoko
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02.109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORMS
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                         PRICA APELICATION NUMBER: PCT/UP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP /34331
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-MAR.1996
APPLICATION NUMBER: UP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: UP 8/246573
ATTORNEY/AGENT 18-SEP-1996
ATTORNEY/AGENT 18-SEP-1996
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION : UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLGGY: linear MOLECULE TYPE: protein FRAGWENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Masato
APPLICANT: Mority, Takeo
APPLICANT: Mority, Takeo
APPLICANT: Mishimura, Osamu
TITLE OF INVENITON: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHWAN, LLP.
STREET: 130 Water Street
CITY: Boston
STATE: Ma
COUNTRY: Boston
STATE: Ma
COUNTRY: Boston
STATE: Ma
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC COMPATIBLE
ADDITORING NUMBER: US/09/105,678A
FILING DATE: 26-UNN-1998
PRICATION NUMBER: US/09/105,678A
FILING DATE: 26-UNN-1997
FILING DATE: 27-UNN-1997
FILING DATE: 27-UNN-1997
FILING DATE: 27-UNN-1997
FILING DATE: 27-UNN-1997
FILING DATE: 27-UNN-1097
FILING DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 109; DB 3; Length 22;
Pred. No. 8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1) Score 109; DB 11arity 100.0%; Pred. No. 8e-Conservative 0; Mismatches
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09105678A Patent No. 6103882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPDINPAWYAGRGIRPVGR 19
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 22 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserva
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99.1%; Score 109; DB 3; Length 31;

Query Match

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August 12, 2004, 14:37:36 ; Search time 5.74419 Seconds (without alignments) 217.697 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                     283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                    US-09-700-643A-1_COPY_12_24
78
1 TPDINPAWYAGRG 13
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
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                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	~	hypothetical prote	ž	hypothetical prote	딤	급	4.		cytochrome-c oxida		probable transport	probable transport	hypothetical 41.1K	related to BCS1 pr	hypothetical prote		Proclavaminic acid	c	cal pr	probable amino aci	inner	inner membrane tra	related to trichod	hypothetical prote	D	hepatocyte growth	conserved hypothet	endo-xyloglucan tr	conserved hypothet
9		9	T33175	20	96	78	AH3166	B37222	T47548	866600	E87151	F91173	F86019	S47704	T49717	B72621	H84384	857669	I50702	AE2349	G64720	G90629	G85480	T51214	E83144	OYURGA	T30811	$\sim$	T51754	G75570
DB		N	0	Н	~	~	N	~	~	~	N	~	(7)	~	(7	~	~	Н	7	~	(7)	N	7	(7)	(7)	Н	N	~	~	Ŋ
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% Query Match		**	٠	Ċ	7.	ın	ın.	'n.	'n	ë.	ω.	'n	m.	ω.	w.	ď	ď	ď	ď.	ά.	ď	ď.	ζ.	ď.	4	ď	52.6	ä	ij	Η.
Ω. σ.	) ) ; ) ) ; ) ; ) ;	74	20	47	45	44	43	43	43	42	42	42	42	42	41.5	41	41	41	41	41	41	41	41	41	41	41	41	40.5	40	40
Result	; ;	г	7	m	4	S	Ģ	7	<b>c</b> c	6	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	28	29

xyloglucan endo-1,	cysteine synthase	drebrin - chicken	drebrin E2 - chick	hypothetical prote	oxoglutarate dehyd	probable magnesium	probable polyketid	probable polyketid	elastic titin - hu	RVS167 protein - y	bacterioferritin c	hypothetical prote	regulatory protein	hypothetical prote	integrase - Mycoba
861555	G82844	I51213	A43776	A84089	A38234	T31462	T03222	T03223	I38346	S40887	G75424	T28762	S12643	G84362	S22643
N	N	N	N	N	N	7	7	7	7	,~1	7	7	0	~	7
269	390	593	607	957	1003	1292	1762	2100	7962	482	163	176	294	325	333
m	1.3	51.3	51.3	51.3	51.3	51.3	51.3	51.3	51.3	50.6	50.0	50.0	50.0	50.0	50.0
51.	u,														
40 51.		40	40	40	40	40	40	40	40	39.5	39	39	39	39	39

### ALIGNMENTS

RESULT 1 JC7607

JC7607 prolactin-releasing peptide - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7607 R;Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T
Biochem. Biophys. Res. Commun. 281, 53-56, 2001 a.mitle: Isolation and characterization of the rat prolactin-releasing peptide gene: Mul
A; Reference number: JC7607; MUID:21092785; PMID:11178959
A;Contents: Spleen A;Accession: UC7607
A;Molecule type: DNA A;Residues: 1-83 <yam></yam>
release, and stimulation of ACTH secretion from the pituitary. CyGenetics: A;Gene: PrRP A;Introns: 33/1
Match 94.9%; Score 74;
<pre>Best Local Similarity 92.3%; Pred. No. be-05; Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</pre>
Cy 1 TPDINPAWYAGRG 13 (
Db 33 TPDINPAWYTGRG 45
hypothetical protein C24G6.6 - Caenorhabditis elegans
Cibpectes: camodinabaturs eregans Cibbte: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 Cibbonian: m3175
V,Accession: 13-11. R,Greco, T.; Bradshaw, H.; Keppler, D.
submitted to the EMBL Data Library, May 1998 ***********************************
Z21298
A,Accession: T33175 A,Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA A: Residnes: 1-527 <gre></gre>
Ajūrosiucos: 1.27, 2012. Ajūrose-references: EMBL:AF067936; PIDN:AAC19213.1; GSPDB:GN00023; CESP:C24G6.6 AjExperimental source: strain Bristol N2; clone C24G6
C;Genetics: A;Gene: CESP:C24G6.6
Ajudp position: 5 Ajintrons: 20/3; 77/1; 129/2; 208/3; 470/2
Query Match 64.1%; Score 50; DB 2; Length 527;

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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N., M.; Koo, H.; Mcffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
Affilte: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CjAccession: AH1166
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. Rarge, G.; Gillet, W.; Seruta, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oytochrome P450 1A2, hepatic - dog
Oytochrome P450 1A2, hepatic - dog
NiAlternate names: cytochrome P450 (Dah2); cytochrome P450-D3
NiAlternate names: cytochrome P450 (Dah2); cytochrome P450-D3
NiOntains: oxidoreductase (EC. 1-..-)
C;Species: Canis lupus familiaris (dog)
C;Date: 31-Mar-1992 #sequence_revision 01-Mar-1996 #text_change 04-Mar-2000
C;Date: 31-Mar-1992 #sequence_revision 01-Mar-1996 #text_change 04-Mar-2000
R;Uchida, T: Komori, M: Ktada, M: Kamataki, T.
Mol. Pharmacol: 38, 644-651, 1990
A;Title: Isolation of cDNAs coding for three different forms of liver microsomal cytochroman difference number: A37222; MUID:91042464; PMID:2122230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein ugpB [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pl. C;Species: Agrobacterium tumefaciens
C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-419 <KUR>
A;Cross-references: GB:AE008687; PIDN:AAL45750.1; PID:g17743483; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                    A;Residues: 1-398 <STO>
A;Cross-references: GB:AE002093; NID:94581140; PIDN:AAD24624.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 2;
Pred. No. 17;
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Pred. No. 27;
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        56.4%;
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46.2%;
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Matches 7; Conserv
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                         A;Status: preliminary
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A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                               A; Molecule type: DNA
    C84780
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A;Map position: 2
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A;Genome: plasmid
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       C; Accession:
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A;Map position: 4
A:Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1;
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A;Experimental source: clone F38E11
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypochetical protein F38E11.7 - Caenorhabditis elegans
C'Species: Caenorhabditis elegans
C'Jate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C'Accession: T21969
R'Matchews, P.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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Pred. No. 6.1;
0; Mismatches 2; Indels
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                          Indels
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                        5
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75.0%; Pred. No. 23;
ive 1; Mismatches
  Pred. No. 2.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.3%;
80.0%;
Similarity 66.7
8; Conservative
                                                                                                             370 PNVLSAWYAGRG 381
                                                                    2 PDINPAWYAGRG 13
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Matches 8; Conservative
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Best Local
Matches
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Best Loc Matches

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R;Cole S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, K.M. Raure 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cipecies: Escherichia coli

Cipace: Ba-Ual-2001

Cipacesion: P3-Ual-2001

Cipacession: P3-113

R;Hayasah, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G

R;Hayasah, T.; Makino, K.; Ohnishi, M.; Rurokawa, K.; Ishii, K.; Yokoyama, H.

BNA, Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F91173
probable transporter ECs4358 [imported] - Escherichia coli (strain 0157:H7, substrain RI
                                                                                                                                           A, Genome: mitochondrion
A, Genetic code: SGC4
C; Superfamily: cytochrome-c oxidase chain III
C; Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane
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A;Ressidues: 1-375 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37781.1; PID:g13363832; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-335 <STO>
A;Cross-references: GB:AL450380; NID:g13093596; PIDN:CAC30893.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .ytB homolog [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                Length 311;
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7
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Pred. No. 29;
1; Mismatches
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Pred. No. 35;
4; Mismatches
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C,Superfamily: penicillin tolerance protein
      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-163,'N',165-311 <BRO>
A;Cross-references: EMBL:MB3760
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ilarity 66.7%;
Conservative
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Best Local Similarity 50.0
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         2 PDINPAWYA 10
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
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C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C;Accession: 866600, 828753
R;Hoffmann, R.J.; Boore, J.L.; Brown, W.M.
submitted to the EMBL Date Library, June 1992
A;Reference number: 86600
A;Retrue: preliminary
A;Nolecule type: DNA
A;Catus: preliminary
A;Molecule type: DNA
A;Cross-references: EMBL:M83760; NID:g342485; PIDN:AAA31907.1; PID:g342488
R;Hoffmann, R.J.; Boore, J.L.; Brown, W.M.
Genetics 131, 397-412, 1992
A;Title: A novel mitochondrial genome organization for the blue mussel, Mytilus edulis.
A;Reference number: $28743; MUID:92354892; PMID:1386586
A; Residues: 10-511 <UCH>
R; Ohta, K.; Motoya, M.; Komori, M.; Miura, T.; Kitada, M.; Kamataki, T.
Biochem. Pharmacol. 38, 91-96, 1989
Biochem. Pharmacol. 38, 91-96, 1989
A; Title: A novel form of cytochrome P-450 in beagle dogs. P-450-D3 is a low spin form of A; Accession: A60463; MUD:89087526; PMID:2910310
A; Accession: A60463; MUD:89087526; PMID:2910310
A; Residues: 1-13, 'A', 15-16 <OHT>
C; Genetics
C; Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C; Keywords: chromoprotein; electron transfer; heme; iron; liver; metalloprotein; monooxy
C; Keywords: chromoprotein; electron transfer; heme; iron; liver; metalloprotein; P; 309-475/Domain: cytochrome P450 homology <P453/Binding site: heme iron (Cys) (axial ligand) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F8J2.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47548
R;Nyakatura, G;; Fartmann, B; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner,
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Pred. No. 35;
1, Mismatches 4, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.1%; Score 43; Best Local Similarity 58.3%; Pred. No. 3 Matches 7; Conservative 1; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|| | | |||
121 SPDSGPVWAAGR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 PHHQPSWYWGRG 148
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Search completed: August 12, 2004, 14:50:25 Job time : 6.7419 secs
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Similarity 60.0%;
6; Conservative
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Best Local Similarity 56.2
Matches 9; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                 probable transporter yhh/ [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C/Species: Escherichia coli (Colimported) - Escherichia coli (Species: Escherichia Coli (Species) (Species: Escherichia Coli (Species) (Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: S47/04; Mobiles
R.Flunkett, G.
Submitted to the EMBL Data Library, March 1994
Submitted to the EMBL Data Library, March 1994
Syleference number: S4766
A.Accession: S4770
A.Accession: S4770
A.Molecule type: DNA
A.Molecule type: DNA
A.Rosidues: 1-375 cPLU3
A.Cross-references: EMBL: U00039; NID: 9466582; EIDN: AAB18460.1; FID: 9466621
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A.Filte: The A64720; MUID: 97426617; PMID: 9278503
A.Reference number: A64720; MUID: 97426617; PMID: 9278503
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
S47704
hypothetical 41.1K protein (rhsB-pit intergenic region) - Escherichia coli (strain K-12)
N/Alteriac names: yhhJ protein
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 01-Mar-2002
C;Accession: S47704; H65145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-375 <BLAT>
A;Cross-references: GB:AE00424; GB:U00096; NID:g2367230; PIDN:AAC76510.1; PID:g1789897;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics: A;Gene: yhhJ.
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Pred. No. 35;
4; Mismatches 1; Indels
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Pred. No. 35;
4; Mismatches
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50.0%;
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170 PNLDPAWFGG 179
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170 PNLDPAWFGG 179
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170 PNLDPAWFGG 179
PDINPAWYAG 11
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Matches 5; Conserv
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hypothetical protein APE1427 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: O-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: B72621
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takahawa, B. (1999)
A;Tile: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyra, A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Status: preliminary
related to BCS1 protein precursor [imported] - Neurospora crassa
Nylleanate names: protein B23L21.300
C;Species: Veurospora crassa
C;Date: 02-Un-2000 #sequence_revision 02-Un-2000 #text_change 02-Unn-2000
C;Accession: T49917
R;Schulte, U.; Aign, V.; Hoheisel, U.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z2502
A;Accession: T49717
A;Accession: 
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A;Residudes: 1.156 <KMs.
A;Cross-references: DDBJ.AP000061; NID:g5104821; PIDN:BAA80424.1; PID:g5105110
A;Experimental source: strain Kl
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A;Gene: APB1427
C;Superfamily: Aeropyrum pernix hypothetical protein APB1427
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Pred. No. 17;
1; Mismatches
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escherichia

limulus pol limulus pol mycobacteri schizosacch gallus gall r ectonucle synechococ staphylococ corynebacte vibrio para corynebacte

P77562 P35360 P71555 P71555 O94269 P79995 P97675 Q8dmk6 Q8dmk6 Q83596 Q83596 Q81596 Q81596 Q81596 Q81596

YAIW ECOLI
OPSI LIMPO
OPSI LIMPO
OPSI LIMPO
V955 MYCTU
UBP3 SCHPO
CADA CHICK
NPD3 SYNEL
RJ31 SYNEL
PCP STRAU
PCP STRAU
ISPH UBPH USPH ISPH ISPH ISPH ISPH ISPH

ALIGNMENTS

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777778888888888
   P81264 bos taurus
P81278 rattus norv
P81277 canis famil
P81277 homo sapien
P81293 escherichia
P3193 escherichia
P31819 streptorichia
P31819 streptorichia
P31819 streptorichia
P31819 arbacia pun
P31818 arbacia
                                                                                                                                                                                                             August 12, 2004, 14:37:35; Search time 3.40116 Seconds (without alignments) 199.024 Million cell updates/sec
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                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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SPEB_STRCL
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Listing first 45 summaries
                                                                                                                                                         - protein search, using sw model
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78
1 TPDINPAWYAGRG 13
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Gapop 10.0 , Gapext
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Match Length DB
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Perfect score:
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	\$  	(Froidcill-releasing de PrRP31; Prolactin-		Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea;					Hosoya M., Fukusumi S.,	sekiguchi M.,		1	se and regulates the	Or GERTO, May scrimarace		**************************************	This SWISS-PROT ENERTY IS COPPINGNE. It is produced unrough a collaboration to the cuttoff of bioinformation and the EMRE outstation.	Swiss institute of Biointoimaries and the first of the Bioinformatics Institute. There are no restrictions on its	its content is in no way	Usage by and for commercial	agreement (see nttp://www.isb-sib.cn/announce/ isb-sib.ch),		DASIC	NG PEPTIDE PRRP31.	17 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ROVIDE AMIDE GROUP).	CRC64;	Length 98;	0; Indels 0; Gaps 0;		
98 AA.	ed) sequence update) annotation update)	or (Fike) (sing peptide		ata; Verteb;			23-52.		:	Matsumoto H., S.	he brain.";		(PKL) release	ILS TECEPU PRL.	ongata and	1 ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( ) } { ( )	information	te. There	s long as	removed. U	nt (see ntt		e on pair or	PROLACTIN-RELEASING	TOWGROUP NTT.	AMIDATION (G-54 PROVIDE	5A13B0FA908	78; DB 1; No. 3.18-06;	Mismatches		
PRT;	red) sequence update) annotation updat	le precurs tin-relea		ita; Crani			QUENCE OF	,607765;	i R., Kaw	o T., Mats	otide in t		rolactin z through	n through	edulla obl	440,000,000	copyright.	ice or bro se Institu	tutions a	it is not	se agreeme se@isb-sib	 	l; Cleavage on	PROLAC	PROUPL			08; Score 78;	; ; 0		
STANDARD;	(Rel. 39, Created) (Rel. 39, Last sec (Rel. 41, Last and	-releasing peptid [Contains: Prolac   peptide PrRP20].	(Bovine).	azoa; Chorda leria; Cetart	lae; Bos.	: 51	N.A., AND SE	781; PubMed=9	S., Habata Y., Fuji	suo Y., Asano T.,	releasing per	2-276(1998).	FUNCTION: Stimulates prolactin (	xpression or prolactin actotrophs directly to	SCIFICITY: Me	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Or entry is c	swiss institute Sioinformatic	profit insti	this statemer	s requires a license agreement (; an email to license@isb-sib.ch)	7; BAA29025.1	ation; Signal;	23 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	าง	53	AA; 10544 MW	100.0%	vat	TPDINPAWYAGRG 13	
T 1 BOVIN PRRP BOVIN	P81264; 30-MAY-2000 (F 30-MAY-2000 (F 28-FEB-2003 (F	Prolactin-releasing peptide precursor (FIRV) (F) hormone) [Contains: Prolactin-releasing peptide releasing peptide PrRP20].	PRH. Bos taurus (Bo	Sukaryota; Met Jammalia; Eutl	Bovidae; Bovinae;	NCB1_14X1D=9915; [1]	SEQUENCE FROM N.A., AND SEQUENCE OF	TISSUE=Brain; MEDLINE=98268'	Hinuma S., Habata Y., Fujii R., Kawamata Y	Kitada C., Mar	"A prolactin-	77	-!- FUNCTION:	expression lactotrop		COC CO FEED - 7 7 FE	Inis SWISS-PR	the European	-uou kq	modified and	entities requires or send an email t	EMBL; AB015417; BAA29025.1	Hormone; Amid	PEPTIDE	PEFILUE		SEQUENCE 98	Query Match	3;	1 TPDI	34 TPDI
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P81277:
                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN-Spraque-Dawley, TISSUE-Hypothalamus;
Anderson S.T., Kokay, I.C., Lang T., Grattan D.R., Curlewis J.D.;
"Quantitation of prodactin-releasing peptide (PrRP) mRNA expression in specific brain regions during the rat oestrous cycle and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION (G-53 PROVIDE AMIDE GROUP).
TPDINPAWYTGRGIRPVGRPGRRRATPRDVTGLGQLSCLPL
DGRTKFSQRG -> SECLTYGKQPLISFHPPTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY.
MEDLINE=99426652; PubMed=10498338;
Pujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
                PRRP_RAT

AC P81279; 0883Y0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-PFB-2003 (Rel. 41, Last annotation update)
DT 28-FFB-2003 (Rel. 41, Last annotation releasing be prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing DE hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sumino Y., Fujino M.; "Tissue distribution of prolactin-releasing peptide (PrRP) and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isold=P81278-2; Sequence=VSP 004370;
TISSUE SPECIFICITY: Widely expressed, with highest levels in
medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMB1; AFD21330; CAUGEDONS SIGNAL Cleavage on pair of basic residues; Alternative splicing.
Alternative splicing.
SIGNAL 1 21 BY SIMILARITY.
PEPTIDE 22 52 PROLACTIN-RELEASING PEPTIDE PRRP31 PROLACTIN-RELEASING PEPTIDE PRRP31 PROPIDE 33 52 PROLACTIN-RELEASING PEPTIDE PRRP30 PROPED 57 83 AMIDATION (G-53 PROVIDE AMIDE GROUND RES 52 52 AMIDATION (G-53 PROVIDE AMIDE GROUND RES 52 52 TPDINFAWYTGRGIRPUGRGRRATPRIVITGIC NARRAPLIC 33 83 TPDINFAWYTGRGIRPUGRGRRATPRIVITGIC NARRAPLIC SAGELTYGRQPLISFHPPFISC
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98268781; PubMed=9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Ful-
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-relasing peptide in the brain.";
Nature 393:272-276 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lactation.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lsoId=P81278-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB015418; BAA29026.1; -.
EMBL; AF521930; AAM82154.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regul. Pept. 83:1-10(1999).
                                                                                                                                                                                                    releasing peptide PrRP20].
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Programmer of the projection (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.

-1- TISSUE SPECIFICITY: Medulla oblongata and hypothalamus.
                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99426652; PubMed=10498338; Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S. Sekjauchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sumino Y., Fujino M., "Tissue distribution M.; and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2003 (Rel. 41, Last amoutation update)
Prolactin-releasing peptide precursor (PRRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PRRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION (G-54 PROVIDE AMIDE GROUP)
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PROLACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDDINE=99268781; PubMed=9607765;
Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Ful
Kitdada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
Nature 393:272-276(1998).
                                                                                                                 Score 74; DB 1; Length 83; Pred. No. 1.2e-05;
                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72; DB 1; Length 87; Pred. No. 2.8e-05; 0; Mismatches 1; Indels
isoform 2).
/FTId=VSP 004370.
DOC75A264EEE4F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229A2F3F50CF981B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         87 AA.
                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB015419; BAA29027.1; -.
                                                          9215 MW;
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                                                                                                                                                                                                                                   1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                        33 TPDINPAWYTGRG 45
                                                                                                                 Query Match
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                             83 AA;
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STANDARD;

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C STRAIN=IN;

K ROLINE=2.1123432; PubMed=11234002;

K ROLINE=2.112313; PubMed=11234002;

Cole S.T. Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,

Medeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

Mungall K., Baedam D., Brown D., Chillingworth T., Connor R.,

Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,

Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

Massive gene decay in the leprosy bacillus.";

Nature 409:1007-1011(2001). Nature 409:1007-1011(2001).

-!- FUNCTION Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) (By similarity).

-!- CATALYTIC ACTIVITY: Isopentenyl diphosphate + NAD(P) (+) + H(2) 0 = (E) 4-hydroxy-3-methylut-2-en-1-yl diphosphate + NAD(P)H. 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2001 (Rel. 42, Last annotation update)
110-OCT-203 methylbut-2-enyl diphosphate reductase (EC 1.17.1.2)
1SPH OR LYTB OR LYTB2 OR ML1938 OR MLCB1222.06C. Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium. (last) step.
-!- SIMILARITY: Belongs to the ispH family. Mycobacterium leprae. NCBI_TaxID=1769; MYCLE ISPH MYC Q9X781; ISPH MYCLE
AC DISPH MY AC DISPH AC D g REPUBLICE OF 1-16.

REPUBLIA SEGUENCE OF 1-16.

REPUBLIA SEGUENCE OF 1-16.

REPUBLIA SEGUENCE OF TISSUE-Liver;

REPUBLIA SEGUENCE SEGUENCE SEGUENCE STRAIN-SEGUENCE SUBSISSES SEGUENCE 453 453 IRON (HEME AXIAL LIGAND) (BY SIMILARITY) 511 AB; 57505 MW; 200904C54F4B3CE7 CRC64; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 28-PEB-2003 (Rel. 41, Last notation update) Cytochrome P450 1A2 (EC 1.14.14.1) (CYPIA2) (DAH2) (Cytochrome P450-STRAIN=Beagle; TISSUB-Liver;
STRAIN=Beagle; TISSUB-Liver;
MCBLINE=20142346, PubMed=212230;
WChida T., Komori M., Kitada M., Kamataki T.;
"Isolation of cDNAs coding for three different forms of liver microsomal cytochrome P-450 from polychlorinated biphenyl-treated beagle dogs.";
Mol. Pharmacol. 38:644-651(1990). Canis familiaris (Dog). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis. NCBI_TaxID=9615, 55.1%; Score 43; DB 1; Length 511; 58.3%; Pred. No. 11; ive 1; Mismatches 4; Indels Query Match
Best Local Similarity 58.33,
Best Local Similarity 58.33, 34 TPDINPAWYASRG 46 STANDARD; CANFA SEQUENCE RESULT 4

CP12 CANNA
AC PS6521;
DT 15-DEC-1;
DT 15-DEC-1;
DT 28-FBB-2;
DE CYLCCPTO
DE CYLCCTO
DE CYLLAZ.
CGN CANNA
AN (1)

RP SEQUENCE
RX MEDLINE BR
RX MACCOSONG
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RX MITT METALINE
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EMBL; AL049491; CAB39812.1; ALT_INIT.
EMBL; ALS83923; CAC30893.1; ALT_INIT.
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                                                                   Leproma; MI1938; -..
HAMAP; MF 001911; -; 1.
InterPro; IPR00345; LivEB.
Pfam; PF02401; LYTE; 1.
TIGREPAMs; TIGRA00216; ispH 1ytE; 1.
Isopreme biosynthesis; Complete proteome; Oxidoreductase; NADP.
SEQUENCE 332 Aa; 36225 MW; F2A82A06EEC35E13 CRC64;
                                                                                                                                                                                                                                      Length 332;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                YHJ ECOLI STANDARD; PRT, 374 AA.

TO YHJ ECOLI STANDARD; PRT, 374 AA.

C P31993; P76703;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypotherical protein yhhd.
GN YHH OR B3485 OR SF3501 OR 54262.
OS Escherichia coli, and
                                                                                                                                                                                                                                    53.8%; Score 42; DB 1;
77.8%; Pred. No. 11;
iive 1; Mismatches 1
                                                                                                                                                                                                                                                                                     Conservative
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270 DIDPAWLAG 278
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Best Local Similarity
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1 TPDINPAWYAGR 12

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                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                  SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniela D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential).
-!- SIMILARITY: Belongs to the ABC-2 integral membrane protein family.
-!- SIMILARITY: TO E.COLI YBHR AND YBHS AND TO THE C-TERMINAL OF
E.COLI YHIG.
                                                                                                                                                                                                                                                                                                            SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin C., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin C., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                               SPECTES=E.coli, STRAIN=K12;
MEDINE=2925920; PubMed=6387990,
Zhao S., Sandt C.H., Feulner G., Vlazny D.A., Gray J.A., Hill C.W.;
"Rhs elements of Escherichia coli K-12: complex composites of shared
and unique components that have different evolutionary histories.";
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Infect. Immun. 71:2775-2786(2003).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22590274; PubMed=12704152; Wei J. Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., Runyen-Janecky L.J., Zhou S., Complete genome sequence and comparative genomics of Shigella flexner; scrotype Za strain Z457T."; Infect. Immun. 71:2775-2786 (2003):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000412; ABC transpt2.
PROSITE; PS00890; ABC2 MEMBRANE; 1.
Hypothetical protein; Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
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POTENTIAL.
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EMBL; AE000444; AAC76510.1; ALT_INIT.
EMBL; L02370; AAC61886.1; -
EMBL; AE015358; AAN44960.1; ALT_INIT.
EMBL; AE016992; AAP19222.1; -.
                                                                                                                                                                                    SEQUENCE OF 225-374 FROM N.A.
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250
276
304
363
                                           NCBI_TaxID=562, 623;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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IRANSMEM 23
 Shigella flexneri
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                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fosberry A., Rawlinson N.S., Ross H.N.M., Neal R.J.,
                                                                                                                                                                                                                                                                                                  SPEB STRCL STANDARD, PRT; 313 AA.
P37819; P72400;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Possible agmatinase (EC 3.5.3.11) (Agmatine urechydrolase) (AUH)
(Proclavaminic acid amidino hydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=4ATC 27064 / DSM 738 / NRRL 3585;
MEDLINE=94374706; PubMed=808847;
Aidoo K.A., Wong A., Alexander D.C., Rittammer R.A.R., Jensen S.
"Cloning, sequencing and disruption of a gene from Streptomyces
clavuligerus involved in clavulanic acid biosynthesis.";
Gen 147:41-46(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MANGANESE 1 (BY SIMILARITY).
NANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
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                                          Score 42; DB 1; Length 374;
Pred. No. 12;
4; Mismatches 1; Indels
  02895FB13F493391 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, U87786; AAA62451.1; -.
EMBL, X84101; CAA58904.1; -.
PIR, S57669; S57669.
PDB, 1GQ6; Z6-UN-03.
PDB; 1GQ7; Z6-UN-03.
INTERPORT PROUS925; Agmatinase.
INTERPORT PROUS925; Arginase.
INTERPORT PROUS925; Arginase.
PROUSPS PROUS91; arginase; I.
PRIWYS; PROUS16; ARGINASE.
TICRFAMS; TICRO1230; agmatinase; I.
PROSITE; PS00148; ARGINASE 2; I.
PROSITE; PS00148; ARGINASE 2; I.
PROSITE; PS00148; ARGINASE 2; I.
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METAL
41061 MW;
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                                             53.8%;
ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces clavuligerus.
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169 PNLDPAWFGG 178
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148
235
237
                    Query Match
Best Local Similarity
"...a 5; Conserv
                                                                                                                                          2 PDINPAWYAG
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146 1
148 1
235 2
237 2
313 AA;
  374 AA;
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Length 391;

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Query Match
                                                                                                                                                      RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and ovary.

-!- PRYELOPMENTAL STAGE: Initially transcribed in the cardiac crescent prior to formation of the primordial heart tube. Following formation of the primitive heart, present in both endocardium and myocardium as well as in other lateral plate derivatives. Also transcribed in the primitive embryonic gut and in late stage embryos is sequentially up-regulated in distinct segments of gastroincestinal epithelia as they undergo terminal differentiation.

-!- SIMILARITY: Contains 2 GATA-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=White leghbrn,
MEDLINE=9455018; PubMed=8083222;
Laverriere A.C., Machell C., Mueller C., Poelmann R.E.,
Burch J.B.E., Evans T.;
Burch J.B.E., Evans T.;
Laverloping heart and gut.",
J. Biol. Chem. 269:23177-23184(1994).
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: More abundant in stomach and small intestine,
lower levels in heart, lung and spleen. Very low levels in liver
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U11888; AAA57504.1; -.
R HISP, 150702; 150702.
R HSSP, P17679; 1GNF.
R TRANSFAC; 1PR008013; GATA-N.
R INTEAPTO; 1PR008013; GATA-N.
R INTEAPTO; 1PR00679; ZNF GATA.
R PÉMN; PF00320; GATA.2.
R PÉMN; PF00320; GATA.2.
R PRINTS; PR00619; GATAZNFINGER.
R SMAPT; SN004014; ZNF GATA. ZN FINGER. 1; 2.
R PROSITE; PS50114; GATA_ZN FINGER. 2; 2.
R PROSITE; PS50114; GATA_ZN FINGER. 2; 2.
R TANSCTÍPLION regulation; Activator; DNA-binding; Zinc-finger;
                                                     ö
                Score 41; DB 1; Length 313;
Pred. No. 15;
                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 GATA-TYPE 1.
263 GATA-TYPE 2.
41858 MW; EF8A283111824260 CRC64;
                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription factor GATA-5 (GATA binding factor-5).
                                                     Mismatches
                  52.6%;
                                     Best_Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210
                                                                                                                        148 DINPAFYGGR 157
                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken)
                                                                                       3 DINPAWYAGR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
239
391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein.
ZN_FING 186
ZN_FING 239
SEQUENCE 391 AA
                                                                                                                                                                                                              CHICK
                  Query Match
                                                                                                                                                                            RESULT 8
GATS_CHICK
ID GATS_CH1
AC P43692;
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                                                   .
0
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIS-RIZ / MG1625.
STRAINS-RIZ / MG1625.
STRAIS-RIZ / MG162.
SIRAIS-RIZ / MG162.
SIRAIS-RIZ / MG162.
SIRAIS-RIZ / MG162.
SIRAIS-RIZ / MG162.
SIRAIS / MG182.
SIRAIS / MG182.
SIRAIS / MG183.
SIRAIS / MG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A., "Systematic sequencing of the Escherichia coli genome: analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS, TIGRO0835; agcS; 1.
PROSITE; PS00873; NA ALANINE SYMP; 1.
Hypothetical protein; Transmembrane; Inner membrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential).
-!- SIMILARITY: BELONGS TO THE SODIUM:ALANINE SYMPORTER FAMILY (SAF). STRONG, TO H.INFLUENZAE H10183.
                                                   .;
0
                                                   Indels
52.6%; Score 41; DB 1;
54.5%; Pred. No. 19;
ive 3; Mismatches 2
                                                                                                                                                                                                                                                                                              TAAJ_ECOLI STANDARD; PRT; 476 AA. P30143; (1-JUL-1993 (Rel. 26, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000111; AAC73118.1; -.
PIR; G64720; G64720.
ECGEne; EG11555; yaad.
InterPro; IPR002283; AA/rel_permeasel.
InterPro; IPR001463; Na/Ala_symport.
Pfam; PP01235; Na Ala_symp; 1.
PRINTS; PR00175; NAALASMPORT.
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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Nucleic Acids Res. 20:3305-3308(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12;
MEDLINE=92334977; PubMed=1630901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Escherichia
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D10483; BAB96585.1; -.
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TRANSMEM 4 24
                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative transporter yaaJ.
                                                         Conservative
                                                                                                                                                             139 TPELPPSWTAG 149
                                                                                                          1 TPDINPAWYAG 11
                         Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAAJ OR B0007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Testis;

X MEDLINE=88318927; PubMed=2901039;

A Singh S., Lowe D.G., Thorpe D.S., Rodriguez H., Kuang W.-J.,

A bangott L.J., Chinkers M., Goeddel D.V., Garbers D.L.;

XT Membrane guanylate cyclase is a cell-surface receptor with homology

XI Membrane guanylate cyclase is a cell-surface receptor with homology

XI Membrane guanylate cyclase is a cell-surface receptor with homology

XI Membrane guanylate cyclase is a cell-surface receptor with homology

XI New Preserver W. A. Chinkers M. M. M. Warlows O'THER CELLS

CC -! FUNCTION: IMPLICATED AS A CELL-SURFACE RECEPTOR ON SPERMATOZOA

FOR RESACY A CHEMOTACTIC PEPTIDE.

CC -! CATALYTIC ACTIVITY: GTP = 3', 5'-cyclic GMP + diphosphate.

CC -! CATALYTIC ACTIVITY: GTP = 3', 5'-cyclic GMP + diphosphate.

CC -! SUBCELLUAR LOCATION: Type I membrane protein.

CC -! SIMILARITY: Contains 1 protein kinase-like domain.
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                 Resact receptor precursor (Guanylate cyclase) (EC 4.6.1.2).
Arbacia punctulate (Punctuate sea urofiln).
Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoldea; Echinacea; Arbacoida; Arbaciidae; Arbacia.
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CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE LIKE.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
S4 MW; B40238A74CCAFCS2 CRC64;
                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodom, PD00000î; Prot kinase; 1.
PROSITE, PSS0011; PROTĒIN KINASĒ DOM, 1.
Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
GMP biosynthesis; Signal.
                                                                                            Score 41; DB 1; Length 476; Pred. No. 23;
                                                                                                                               2; Indels
 371 POTENTIAL.
411 POTENTIAL.
POTENTIAL.
51662 MW; 2F6EB2E12E12EE63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESACT RECEPTOR.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                         01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                             986 AA
                                                                                        Query.Match 52.6%; Score 41; DB Best Local Similarity 47.1%; Pred. No. 23; Matches 8; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X12874; CAA31367.1; -.
PIR, S05480; OYURGA.
InterPro; IPR001828; ANF receptor.
InterPro; IPR001054; G_Cyclase.
InterPro; IPR000719; Prot kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01094; ANF receptor; 1.
Pfam; PF00211; guanylate cyc; 1.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                    120 DVNGQFRGGPAWYMARG 136
                                                                                                                                                               3 DIN-----PAWYAGRG 13
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                                                                                                                                                                                                                                                                                             STANDARD;
 351 3
391 4
414 4
476 AA;
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185
361
410
986 AA;
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                 TRANSMEM
TRANSMEM
                                                     SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Hafe D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Noffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makazova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                           15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
NAD-dependent deacetylase (EC 3.5.1.-) (Regulatory protein SIR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the radioresistant bacterium Deinococcus
   Score 41; DB 1; Length 986;
Pred. No. 47;
                                                                                                                                                                                                                                                                                   Deinococcus radiodurans.
Bacteria; Deinococcus-Thermus, Deinococci; Deinococcales;
Deinococcaccae. Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.3%; Score 40; DB 1; Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEACETYLASE SIRTUIN-TYPE.
NAD BINDING (BY SIMILARITY).
BY SIMILARITY.
                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6B97C73D7D98B34D CRC64;
                                                                                                                                                                  246 AA.
                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase, NAD, Complete proteome.
DOMAIN 4 246 DEACE
                                                                                                                                                                                           15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last seq
15-MAR-2004 (Rel. 43, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001865; AAF09608.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR, DR0016; -...
HAMAR, MF 01121; -; 1.
INTERPRO; IPR003000; SIR2.
PEam; PF02146; SIR2; 1.
PROSITE; PS50305; SIRTUIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 AA; 26457 MW;
   52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.68;
Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PDINPAWYAGR 12
                                                                                         475 PDLNPVWH 482
                                                           2 PDINPAWY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IR; G75570; G75570.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       homolog).
NPDA OR DR0016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M.;
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SEQUENCE
                                                                                                                                                                             Q9RYD4;
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59 PDLVWEWYAGR 69

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RESULE FROM N.A.

RESULES COLUMDA.

RESULES COLUMDA.

RESULES COLUMDA.

RESULES COLUMDA.

RESULES COLUMDA.

RESULES EV. ALGEBERGE M., ENTAGE N. P. BRITAN K. -D. TETTYN N.

RESULES EV. ABOOTGE M., Estand P., Caivell L.A., Rieger M.,

RESULES EV. ABOOTGE W., Enand P. Caivell L.A., Rieger M.,

RESULES EV. ABOOTGE W., Endelle T. A., Rieger M.,

RESULE M. Delseartner M., de Simone V., Obermaier B. Mache R., Mueller M.,

Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

RA Vos P., Hobisel J., Zimmerman W., Medler H., Rolley P.,

Langham S.-A., McCullagh B., Bilham L., Robben J.,

Langham S.-A., McCullagh B., Bilham L., Robben J.,

Reichert B., Roilens I., Coff W., Bastiens I., Aert R., Defcor E.,

RA Worles S. Hemine S., Rose M., Hauf J., Koetter P.,

RA Holzer S., Hempel S., Feldpausch M., Lamberth S., Van den Bele H.,

RA Montagor T., Buyesheart C., Gielen J., Villarroel R., De Clercq R.,

RA Montagon M., Rogers J., Cromin A., Ouail M.N., Bray-Allen S.,

RA Montagon M., Rogers J., Cromin A., Ouail M.N., Bray-Allen S.,

RA Pettett A., Rajandream M., Marke M., Rechmann S.,

RA Pettett A., Rajandream W., Marke M., Rechmann S.,

RA Pettett A., Rajandream W., Marke M., Rechmann S.,

RA Borkova D. Bloceker H., Schaefe M., Mueller-Auer S.,

RA Borkova D., Blocker H., Schaefe M., Mueller-Auer S.,

RA Gebel C., Fuchs M., Fartmann B., Grandcath M., Melnard M., Aubourg S.,

RA Gebel C., Fuchs M., Fartmann B., Grandcath M., Raber S.,

RA Gibbons T., Wandenbol M., Bargues M., Relber S.,

RA Gibbons T., Wandenbol M., Bargues M., Rachmann S.,

RA Grand D., Hasse D., Lamke K., Gorder S.,

RA Arcelliu L., Dedhia M., Mison R.K., de la Bastide M., Habermann R.,

RA Bernelses D., Lemke K., Johnson S., Tacon D., Joese T.,

RA Bernelses D., Lemke K., Wewes H. W., Stocker S.,

RA Arcelliu L., Dedhia M., Marson R., Remp K., Hiller M., Scott K., Johnson D.,

RA Arcelliu P., Couttrey U., Fulton B., Miller M., Bernel M., Miller M., Scott K., Cotten M., Delber S., Balder S., Gelbel D., RA, Minx P., Bentley D., Fulton B., M
                                            TY24 ARATH STANDARD; PRT; 269 AA.

AC P24876; O64956; Q39148; Q39149; Q41904; Q8LDQ0;

AC P24876; O64956; Q39148; Q39149; Q41904; Q8LDQ0;

AC P24876; O64956; Q39148; Q39149; Q41904; Q8LDQ0;

DT 01-MAR-1992 (Rel. 21, Created)

DT 28-FEB-2003 (Rel. 44) Last sequence update)

DT 15-MAR-2004 (Rel. 43) Last sequence update)

DT 15-MAR-2004 (Rel. 44) Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medford J.I., Elmer J.S., Klee H.J.;
"Molecular cloning and characterization of genes expressed in shoot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Columbia;
Kamimai T., Tomita E., Nishitani K.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93005704; PubMed=1840916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Cell 3:359-370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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RESULT 12

TY124 ARATH

ID X7124 ARATH

ID X7124 ARATH

ID X24876

DT 01-MAR

DT 01-MAR

DE CO 20

DE CO 20

DE CO 20

DE CO 20

CO SPECIAL

RA MEDUIN

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CV. Columbia;

X MEDLINE=2954860; PubMed=14593172;

X PREDLINE=2954860; PubMed=14593172;

X Vandad K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Cheuk R.F., Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F., A Karlin-Newmann G., Liu S.Y., Lam B., Sakano H., Wu T., Yu G., A Karlin-Newmann G., Liu S.Y., Lam B., Sakano H., Wu T., Yu G., A Chan M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y., A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y., A Chan M., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F., A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Khan S., Koesema E., Vaksjina M., Narlusaka M., Sakurai T., Sakurai T., Satu M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekker M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M.A., Martienssen R., McCombie W.R., "Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENZYMATIC ACTIVITY, AND N-GLYCOSYLATION.
MEDLINE-9934624; PubMed=10406121;
Cambbell P., Bram J.; And J. Cambell P., aream J.;
In vitro activities of four xyloglucan endotransglycosylases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-132 FROM N.A.
STRAIN=CV. Columbia; TISSUE=Green siliques;
MEDLINE=94108489; PubMed=8281187;
Hoefte H.R., Desprez T., Amselem J., Chiapello H., Rouze P.,
Hoefte H.R., Desprez T., Gurrion M.-F., Charpenteau J.-L.,
Caboche M., Moisan A., Jourion M.-F., Charpenteau J.-L.,
Thomas F., Yu D.-Y., Mache R., Raynal M., Cooke R., Grellet F.,
Delseny M., Parmentier Y., de Marcillac G., Gigot C., Fleck J.,
Philipps G., Axelos M., Bardet C., Tremousayque D., Lescure B.;
"An inventory of 1152 expressed sequence tags obtained by partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. Columbia; TISSUE=Leaf;
MEDLINE=98278374; PubMed=9617812;
Park V.-H., Oh S.A., Kim Y.H., Noo H.R., Nam H.G.;
Park Ferential expression of senescence-associated mRNAs during senescence induced by different senescence-inducing factors in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arrowsmith D.A., De Silva J.; "Characterisation of two tomato fruit-expressed cDNAs encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DECORTY V., Trockhan M., Alexandrov N., Lu Y.-P., Flavell Brover V., Trockhan M.A.; Feldmann K.A.; Feldmann K.A.; Frill-length CDNA from Arabidopsis thaliana "; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xyloglucan endo-transglycosylase.";
Plant Mol. Biol. 28:391-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol. 37:445-454(1998).
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MEDLINE=21530286; PubMed=11673616;
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MEDLINE=95359399; PubMed=7632911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 104-269 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-120 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 302:842-846(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant J. 4:1051-1061(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lant J. 18:371-382(1999)
                                                                                                                                                                     Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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**Mapline_2740.47; pubMed=12214239;

**Rose J.K.C., Braam J., Fry So. Nishitani K.;

"The XTH family of enzymes involved in xyloglucan endotransglucosylation and endohydrolysis: current perspectives and a new unifying nomenclature.";

"The XTH family of enzymes involved in xyloglucan endohydrolysis (XEH) and/or plant Cell Physiol. 43:1421-1435(2002).

"I PUNCTION: Catalyzes xyloglucan endohydrolysis (XEH) and/or endotransglycosylation (XET). Cleaves and religates xyloglucan polymers, an essential constituant of the primary cell wall, and thereby participates in cell wall construction of growing tissues. Way be required during development to modify the walls of cells under mechanical stress.

"C CATALYTIC ACTIVITY: Breaks a beta-(1->4) bond in the backbone of a xyloglucan and transfers the xyloglucanyl segment on to O-4 of the non-reducing terminal glucose residue of an acceptor, which can be a xyloglucan or an oligosaccharide of xyloglucan.

"SUBCELUTAR LOCATION: Apoplast (Probable).

"I ISSUE SPECIFICITY: Highly expressed in steed in shoot apical meristems, also found in the particular particular particular meristems, also found in the stems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- INDUCTION: May be transcriptionally regulated by ANGUSTIFOLIA.
-!- PTM: Contains at least one intrachain disulfide bond essential for its enzymatic activity (By similarity).
-!- PTM: N-glycosylated; essential for its enzymatic activity.
-!- SIMILARITY: Belongs to family 16 of glycosyl hydrolases. XTH goup 2 subfamily.
-!- GAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 158; 178; 183; 189; 190; 194 and 199.
-!- CAUTION: Ref.6 sequence differs from that shown due to frameshifts in positions 93 and 104.
-!- DATABASE: NAME=XTH-WORLIG;
WWW="http://www.plantbio.cornell.edu/XTH".
                                                                                                                                                                                                            MEDLINE=21886176; PubMed=11889033; Kim G.-T., Zhoda K., Tsuge T., Cho K.-H., Uchimiya H., Yokoyama R., Nishitani K., Tsukaya H.; Tsuge T., Cho K.-H., Uchimiya H., Yokoyama R., "The ANGUSTIFOLIA gene of Arabidopsis, a plant CtBP gene, regulates leaf-cell expansion, the arrangement of cortical microtubules in leaf cells and expression of a gene involved in cell-wall formation."; EMBO J. 21:1267-1279(2002).
Yokoyama R., Nishitani K., "A comprehensive expression analysis of all members of a gene family encoding cell-wall enzymes allowed us to predict cis-regulatory regions involved in cell-wall construction in specific organs of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.3%; Score 40; DB 1; Length 269; 63.6%; Pred. No. 19; 3; Indels ive 1; Mismatches 3; Indels
                                                                                                                                   Plant Cell Physiol. 42:1025-1033(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22402747; PubMed=12514239;
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           NOMENCLATURE
                                                                                                          Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                             Salanoubat M., Genin S., Arriguenave F., Gouzy J., Mangenot S., Arliguenave F., Gouzy J., Mangenot S., Charlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisen N., Claudel-Fenard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Melsenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
-! CATALYTIC ACTIVITY: Coproporphyrinogen-III + O(2) = protoporphyrinogen-IX + 2 CO(2) + 2 H(2)O.
-! COFACTOR: Iron (89 similarity).
-! PATHWAY: Porphyrin biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_0033; -; 1.
InterPro: IPR001260; Coprogen_oxidas.
Pfam; PF01218; Coprogen_oxidas; 1.
PRINTS; PR00073; COPRGNOXDASE; 1.
PROSITE; PR01071; COPRGSEN OXIDASE; 1.
PORPHYIN biosynthesis; Oxidoreductase; Iron; Complete protecome. SEQUENCE 302 AA; 34211 MW; 9BE406E68FDD455B CRC64;
                                                                                                                 Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterineae; Corynebacteriaceae; Corynebacterium,
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)
(Coproporbhyrinogenase) (Coprogen oxidase).
HEMF OR RSC2192 OR RS01407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable exodeoxyribonuclease VII large subunit
(Exonuclease VII large subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.3%; Score 40; DB 1; 50.0%; Pred. No. 21; ive 1; Mismatches
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                                                                                                                                                                                                                              STRAIN=GM11000;
MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Best Local Similarity
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                                                                                                                                                                    NCBI_TaxID=305;
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Q8FQF1;
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Gaps

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Conservative DINPAWYAGRG 13 DVNVAWGNGRG 37

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ò g 302 AA.

PRT;

RESULT 13.
HEM6 RALSO STANDARD; I AC Q8XXC3; BT 28-FEB-2003 (Rel. 41, Created)

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Job time : 4.40116 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.", Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Baidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid-soluble oligonucleotides (By similarity).
-!- CAPALYTIC ACTIVITY: Exonucleolytic cleavage in either 5' to 3'-
or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
-!- SUBUNIT; Heterooligomer composed of large and small subunits (By
                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
(Exonuclease VII large subunit).
 Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.3%; Score 40; DB 1; Length 413; 87.5%; Pred. No. 29; 0; Indels iive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase, Nuclease, Exonuclease, Complete proteome.
SEQUENCE 413 AA, 45171 MW; D3BABD9687C6EE5D CRC64;
                                                                                                                                                                                            similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the xseA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
-!- SIMILARITY: Belongs to the xseA family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF 00378; -; 1.
InterPro; IRR003753; Exonuc VII b.
InterPro; IRR008994; Nucleic_acid_OB.
Pfam; PF02601; Exonuc VII L; 1.
IIGRFAMS; TIGR00237; XSeA; 1.
                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP005217; BAC17888.1; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 51.3
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 PAFYAGRG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 PAWYAGRG 13
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                                 Gojobori
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QBNRM3;
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sion 5.1.6	Copyright (c) 1993 - 2004 Compugen Ltd.	
GenCore version 5.1.6	: (c) 1993 - 20	
	Copyright	

August 12, 2004, 14:37:35 ; Search time 17.9128 Seconds (without alignments) 228.984 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-700-643A-1_COPY_12_24
78
1 TPDINPAWYAGRG 13 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapext 0.5

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL 25:*

1: Sp_archea:*
2: Sp_archea:*
3: Sp_fungi:*
4: Sp_fungi:*
5: Sp_invertebrate:*
6: Sp_invertebrate:*
7: Sp_invertebrate:*
8: Sp_onganelle:*
9: Sp_onganelle:*
10: Sp_lant:*
10: Sp_lant:*
10: Sp_lant:*
2: Sp_virus:*
3: Sp_virus:*
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5: Sp_virus:*
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6: Sp_virus:*
7: Sp_virus:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q8wn12 ovis aries	Q9w624 carassius a	Q7z6yl homo sapien	O60687 homo sapien	Q8ww85 homo sapien	076383 caenorhabdi	Q8r054 mus musculu	Q8k1f8 mus musculu	O27142 methanobact	Q886t3 pseudomonas	Q20170 caenorhabdi		Q98mb6 rhizobium l	Q8alv0 bacteroides	Q9sjr5 arabidopsis	Q8gys6 arabidopsis
	ΔI	Q8WN12	Q9W624	Q7Z6Y1	060687	QBWW85	076383	Q8R054	QBK1F8	027142	Q886T3	020170	Q91FX2	98MB6Q	Q8A1V0	Q9SJR5	Q8GYS6
	DB	9	13	4	4	4	Ŋ	11	11	17	16	ഗ	12	16	16	10	10
	Query Match Length DB	86	117	54	465	465	527	467	468	430	540	179	472	369	379	398	398
æ	Query Match	100.0	70.5	67.9	67.9	67.9	64.1	61.5	61.5	60.3	60.3	57.7	57.7	56.4	56.4	56.4	56.4
	Score	78	55	53	53	53	50	48	48	47	47	4.5	4. N	44	44	44	44
	Result No.	1	(7)	m	4	ស	9	7	œ	σ	10	11	12	13	14	15	16

	ω ⊸	0 arabidops	7 arabidops		Q8ukp2 agrobacteri					Q8p3n1 xanthomonas	Q8pf24 xanthomonas	Q9nxs8 homo sapien	Q8zxh2 pyrobaculum	Q8ivg6 homo sapien	Q9td69 mytilus cal	Q85r31 mytilus tro	Q82rv0 streptomyce	Q8xvh7 ralstonia s		Q8zle1 salmonella		~		Q88rq2. pseudomonas	н	O9rmjo neisseria m		Q9p5j9 neurospora	
Q7XMH8	Q7U4H3	Q84WL0	Q8L8A7	Q7VUL5	Q8UKP2	Q7WQX8	Q7W200	Q8JI36	Q9LFA0	Q8P3N1	Q8PF24	8SXN6Ö	Q8ZXH2	QBIVG6	Q9TD69	Q85R31							Q88B54		Q9RMJ1	Q9RMJ0	6	Q9P5J9	
10	16	10	10	16	16	16	16	13	10	16	16	4	17	4	œ	æ	16	16	16	16	16	16	16	16	α	7	16	m	
816	98	6	380	387	419	432	3	501	4	605	Н	630		1595	72	120	130	211	341	374	375	402	501	505	548	548	694	779	
56.4	55.1	10	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	55.1	53.8	м М	53.8	53.8	53.8	ω.		53.8	53.8	53.8	53.8	53.8	53.8	•	
44	43	43	43	43	43	43	43	43	43	43	43	43	43	43	42	42	42	42	42	42	42	42	42	42	42	42	42	41.5	
17	8	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45	

## ALIGNMENTS

RESULT 1 QBWN12	ID Q8WN12 PRELIMINARY; PRT; 98 AA. AC 08WN12;	2002				OS Ovis aries (Sheep).			OC Bovidae; Caprinae; Ovis.	OX NCBI_TaxID=9940;			RA Curlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T.;		RT distribution and effects on prolactin secretion in vitro and in	RT vivo.";		٠	SQ SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAAB5 CRC64;	100.0%; Score 78;	Best Local Similarity 100.0%; Pred. No. 5.5e-05;	Collect vacave of manacolles of the collection	Qy 1 TPDINPAWYAGRG 13	Db 34 TPDINPAWYAGRG 46
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Q9W624 PRELIMINARY; PRT; 117 AA. Q9W624; Q9W624; C1-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) RESULT 2 Q9W624 ID Q9W6; AC Q9W6; DT 01-NC ö

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SEQUENCE FROM N.A.

Huang C.-H., Chen H., Peng J., Chen Y.;

"Cloning and characterization of the sushi-repeat containing protein (SRP) as a novel interaction partner of Rh type C glycoprotein (RRCG).";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Straubberg R.,
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC020733; AAH20733.,
CO; Go:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR003410; Hyalin.
InterPro; IPR003410; Hyalin.
Pfam; PF02494; HyR; 1.
Pfam; PF00084; sushi; 3.
SMARI; SM00032; CCP; 3.
PROSITE; PS00086; CYPOCHROME P450, 1.
SEQUENCE 465 AA; 52957 MW; 3D7229487DA1B8BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.9%; Score 53; DB 4; Length 465; 61.5%; Pred. No. 2.9; 4; Indels ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                  EMBL, AF060567; AACIS765.1; ...
EMBL, AF33649; AAM7363.1; ...
GO, GO:006118; P:01ectron transport; IEA.
InterPro; IPR001129; Cytcohrome_P450.
InterPro; IPR0003410; Hyalin.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF02494; HYR; 1.
Pfam; PF00844; sushi_3.
PROSITE; P$000864; cytCCHROME_P450; 1.
SEQUENCE 465 AA; 52971 MW; 4D752B187FF3EFB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sushi.-repeat protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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01-NOV-1998 (TrEMBLrel. 08, L6
01-OCT-2003 (TrEMBLrel. 25, L8
Hypothetical protein.
C24G6.6.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                       67.9%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.53,
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 TPAVTPTWYAGSG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPDINPAWYAGRG 13
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Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Placenta;
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O76383;
O1-NOV-1998 (
01-NOV-1998 (
01-OCT-2003 (
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076383
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                                             Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE FROM N.A.
Rurosawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T.,
Rakestraw K.M., Naeve C.W., Look T.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
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Best Local Similarity 61.5%; Pred. No. 0.33;
Matches 8; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 54;
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                           TISSUE=Brain;
Satake H., Minakata H., Fujimoto M.;
Carasius RFamide (C-FF amide).";
Carasius RFamide (C-FF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -.
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawlor S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035608; CAB55682.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1993 (TrEMBLrel. 55, Last annotation update)
Sushi-repeat protein (Sushi-repeat containing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DJ47997.3 (Sushl-repeat protein (SRPUL)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 4;
Pred. No. 0.31;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 AA.
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                       Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.5%;
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56 SPEIDPFWYVGRG 68
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                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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060687
10 06068
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Mismatches
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Best Local Similarity 58.3
Matches 7; Conservative
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7; Conservative
                                                                                                   19 PAVTPTWYAGSG 30
                                                                                                                                                                                                                               PRELIMINARY;
                                                   2 PDINPAWYAGRG
                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                1110039C07RIK.
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     Matches
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLOUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to sushi-repeat protein.
1110039C07RIK.
Maks musculus (Mouse).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
111003P0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R;
Strausberg R;
Submitteed (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO28307; AM428307.1; -.
RGD, MGJ:1916042; 1110039C07Rik.
RGJ; GO:0066118; P:electron transport; IEA.
RINterPro; IPR00118; Cytcchrome_P450.
RINterPro; IPR00118; Cytcchrome_P450.
R InterPro; IPR00445; Sushi, SCR_CCP.
R Ffam; PF00084; Sushi, 3.
R PFam; PF00084; Sushi; 3.
R PROSITE; PS00086; CYTCCHROME_P450; 1.
R PROSITE; PS00086; CYTCCHROME_P450; 1.
SEQUENCE 467 AA, 53009 MW; EB4C01C7E6118BE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

64.1%; Score 50; DB 5; Length 527;
Best Local Similarity 66.7%; Pred. No. 10;

Matches 8; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston M2;
Waterston Sinission.";
"Direct Submission.";
"Direct Submission.";
Submitted (SEP-2201) to the EMBL/GenBank/DDBJ databases.
EMBL, AF057936; AAC19213.1;
PIR, T33175.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Greco T., Bradshaw H., Keppler D.;
"The sequence of C. elegans cosmid C24G6.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wormpep, C4466.6; CE17462.

GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR002037; Amino oxidase.
InterPro; IPR000205; NAD NG.
Pfan, PF01593; Amino oxidase; 1.
Hypothetical protein.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.5%; Score 48; DB 11; 58.3%; Pred. No. 18;
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                                                                                                           SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
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Best Local Similarity
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Q8R054;
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Q8R054
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                                                                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A.
TISSUE=Kidner, Peng J., Chen Y.;
"Cloning and characterization of the sushi-repeat containing protein (SRP) as a novel interaction partner of Rh type C glycoprotein
                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

E Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

E MGD; MGI-1916642; Ill003907Rik.

R MGD; MGI-1916642; Ill003907Rik.

R InterPro; IPR001128; Cytochrome_P450.

R InterPro; IPR001128; Cytochrome_P450.

R InterPro; IPR00436; Subhi_SCR_CCP.

R Pfam; PF00494; HYR; J.

R Pfam; PF00494; Bushi; 3.

SMART; SM00032; CCP.

R PROSITE; MG0064; CYTOCHROME_P450; I.

R PROSITE; MG0064; CYTOCHROME_P450; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%; Score 48; DB 11; Length 468; S8.3%; Pred. No..18; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          027142;
01-7AN-1998 (TrEMBLrel. 05, Created)
01-AN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Sushi-repeat containing protein.
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Query Match
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Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
"Complete sequence of Pseudomonas syringae.",
Complete sequence of Pseudomonas syringae.",
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE016861, AAO55014.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
"Complete genome sequence of Methanobacterium thermoautotrophicum deltah: 'Inotional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155 (1997).
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Pred. No. 25;
0; Mismatches 2; Indels
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llarity 70.0%; Pred. No. 31;
Conservative 1; Mismatches 2; Indels
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Last annotation update)
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GO, GO:0016020; C:membrane, IEA.
GO; GO:0004891; F:signal transducer activity; IEA.
GO; GO:0006935; P:chemotaxis; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR004089; Chmtaxis_transd.
InterPro; IPR004089; MaMP.
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PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PS50895; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
Methyl-accepting chemotaxis protein.
                                                                                                                                PIR; B69009; B69009.
InterPro; IPR002510; Peptidase_U62.
Pfam, PF01523; PmbA_TldD; 1.
Complete protecome.
SEQUENCE 430 AA; 46062 MW; C4FA
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01-NOV-1996 (TrEMBLrel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                           60.3%;
80.0%;
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Pfam; PF00015; MCPsignal; 1.
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 80.0
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SEQUENCE 540 AA;
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es 7; Conser
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2886713
AC Q886713
DT O1-UDIDT O1-UDID
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Q20170
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SORRERE
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[3]
MEDLINE=87321126; PubMed=2820141;
MEDLINE=87321126; PubMed=2820141;
Schnizzler P., Soltau J.B., Fischer M., Reisner H., Scholz J.,
Delius H., Darai G.;
"Molecular cloning and physical mapping of the genome of insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-89073752; PubMed=3201750;
Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive DNA element in the genome of insect iridescent virus type 6.";
Virology 167:485-496(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDMed=1959991;
MEDLINE=86174607; PubMed=1959991;
Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
Insect iridescent virus type 6 induced toxic degenerative hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Delius H., Darai G., Fluegel R.M.;
InDA analysis of insect iridescent virus 6: evidence for circular permutation and terminal redundancy.";
J. Virol. 49:609-614(1984).
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Viruses, dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
NCBI_TaxID=10488;
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
C. elegans WRT-3 protein (Corresponding sequence F38E11.7).
                                                                                                                                                                                                                                                                                      Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z68142; CAA92775.2; -
SEQUENCE 179 AA; 20965 MW; F9FA6891A2BF2BDD CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 5;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 AA
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                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.78;
75.08;
                                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998)
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Virology 160:66-74(1987).
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                                                                                      Caenorhabditis elegans.
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159 PDVKPAWY 166
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SEQUENCE FROM N.A.
MEDLINE=21342569; PubMed=11448171;
Jakob N.J., Muller K., Bahr U., Darai G.;
Jakob N.G., Muller K., Bahr U., Darai G.;
Jakob N.G., Muller K., Bahr U., Darai G.;
Jakob N.G., The First Complete DNA Sequence of an Invertebrate
Iridovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";
Virology 286:182-196(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE=21082930; PubMed=11214968; Kane T., Sasamoto S., Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
          Identification of a gene cluster within the genome of Chilo iridescent virus encoding enzymes involved in viral DNA replication, and processing.";
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.7%; Score 45; DB 12; Length 472; 50.0%; Pred. No. 57;
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Jakob N.J., Mueller K., Bahr U., Darai G.;
Submitred (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF307741; AAK82060.1; -.
SEQUENCE 472 AA; 52183 MW; 8BDF96D987E8F94B CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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DNA Res. 7:331.338 (2000).
EMBL, #0002995, BAB48197.1; -.
INTERPRO, IPR001395, Aldo/Ket_red.
PEAN, PP00248, aldo, Ket_red.
PENUTS, PR00069, ALDKETRDTASE.
PRODOM; PD000288; Aldo/Ket_red; 2.
Muller K., Tidona C.A., Darai G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                        and processing.";
Virus Genes 18:243-264(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 SPSVNPVWVAGO 309
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Matches 6; Conserv
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SEQUENCE 369 AA;
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MEDLINE=93118242; PubMed=1475907;
Sonntag K.C., Darai G.;
"Characterization of the third origin of DNA replication of the genome of insect iridescent virus type 6.";
Virus Genes 6:333-342(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of genes encoding zinc finger proteins, non-histone chromosomal HMG protein homologue, and a putative GTP phosphohydrolase in the genome of Chilo iridescent virus.";
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MEDILINE=943541; PubMed=8073636;
MEDILINE=943541; PubMed=8073636;
Sonntag X.C., Schnitzler P., Koonin E.V., Darai G.;
"Chilo iridescent virus encodes a putative helicase belonging to a distinct family within the 'DEAD/H' superfamily: implications for the evolution of large DNA viruses.";
Virus Genes 8:151-158(1994).
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MEDIJIRE=94502906; PubMed=8021587;
Schnitz=1er P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
Koonin E.V., Darai G.;
"Insect iridescent virus type 6 encodes a polypeptide related to the
"Insect subunit of enkaryotic RNA polymerase II.";
J. Gen. Virol. 75:1557-1567(1994).
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MEDINE=9841633; PubMed=9482589;
MEDINE=9841633; PubMed=9482589;
Bahr U., Tidona C.A., Darai G.;
"The DNA sequence of Chilo iridescent virus between the genome coordinates o.101 and 0.391; similarities in coding strategy between insect and vertebrate iridoviruses.";
virus Genes 15:235-245(1997).
                                                                                                                  "Identification and mapping of origins of DNA replication within the DNA sequences of the genome of insect iridescent virus type 6."; Virus Genes 6:19-32(1992).
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Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
"Identification of the primary structure and the coding capacity of the genome of insect inidescent virus type 6 between the genome coordinates 0.310 and 0.377 (7990 bp).";
intervirology 37:287-297(1994).
                                                   MEDLINE=92196996; PubMed=1549908;
Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93260401; PubMed=8492091; Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.; Stohwasser I., Raab K., Schnitzler P., Janssen W., Darai G.; "Identification of the gene encoding the major capsid protein of insect irideacent virus type 6 by polymerase chain reaction."; J. Gen. Virol. 74:873-879(1993).
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Delius H., Darai C.;
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MEDLINE=99383793; PubMed=10456793;
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SEQUENCE FROM N.A.
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PRELIMINARY;

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Search completed: August 12, 2004, 14:49:00 Job time : 19.9128 secs
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STRAIN=VPI-5482 / ATCC 29148;

X MEDLINE=25550658; PubMed=12663928;

RA Xu J., Bjursell M.K., Himman-Dacteroides thetaiotaomicron symbiosis.";

RA Genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";

RI Science 299:2074-2076(2003).

DR GO; GO:0004519; F:endomuclease activity; IEA.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0001876; F:nucleic acid binding; IEA.

DR Har PPTO: IPRO0164; Endomuclease; 1.

DR SWART; SW00477; NUC; 1.

KW Endomuclease; Complete proteome.

SEQUENCE 379 AA; 41860 MW; 814F834D7D3E0FBB CRC64;
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STRAINS CV. Columbia,
STRAINS CV. Columbia,
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo, H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
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                                                                                               Bacteroides thetalotaomicron,
Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales,
Bacteroidaceae, Bacteroides.
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Pred. No. 65;
1; Mismatches 2; Indels
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                                    Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
At2Q36400 protein (Transcription activator).
AT2G36400 OR GRL3.
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                   Created)
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                ol-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25, PHTARINA CALACTER PHTARIA)
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                                                                Putative endonuclease
BT3558.
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STRAIN=CV. Columbia;
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SEQUENCE FROM N.A.
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Q9SJR5
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Kim J.H., Kende H.; "A novel class of transcription activators interacting with putative co-activators in Arabidopsis."; submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                   Score 44, DB 10, Length 398;
Pred. No. 69;
0, Mismatches 4; Indels
                                                                                                                   398 AA; 43707 MW; 2A6E15497305AF74 CRC64;
                                                                EMBL; AC006919; AAD24624.1; -...
EMBL; AY102636; AAM52878.1; -...
PIR; C84780; C84780.
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Matches 7; Conservative
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Peptide p Peptide p Bovine G Bovine pi Bovine CR Peptide p Bovine GR Bovine GR

Aaw31371
Aaw85188
Aaw95188
Aay49298
Aay49299
Aab10347
Aab60825
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Peptide p Bovine G Bovine pi Bovine pi Bovine pi 19P2 liga 19P2 liga Bovine CK Bovine CK

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This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 34 to 52 of the sequence in AAW31368. This fragment was obtained by purification and analysis of the N-terminal sequence of a P-2 fraction which is used in assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific
                                                                                                                                                                                                                                                                                                           G protein-coupled receptor; ligand binding; pharmaceutical; modulator;
pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by modulating pituitary gland.
                                                                                                                                                                                                                                                                                          Bovine G protein-coupled receptor ligand fragment from P-2 fraction.
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                                AAW97218
AAY49298
AAY49290
AAB10347
AAG62516
AAB26399
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AAW31372
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AAB10348
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AAY49297
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96JP-0059419.
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96JP-00246573.
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                          (first entry)
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N-PSDB; AAV02393.
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28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
18-SEP-1996;
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Bovine G
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Aaw95185 Bovine pi
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Abu6030
Aaw316030
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11: geneseqp1980s:*
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Fukusumi S;

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depression, hyperkinethy and the property of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hypernydrome, schizophrenia, trauma, growth hormone secretory disease, hyperlydragia, hyperprolactinaemia, hyperglyceridaemia, hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, rheumarcid arthritis, spinal injury, transient brain ischaemia, amylotrophic lateral sclerosis, acute myocardial infarction, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein
   prophylactic or therapeutic agent for dementia,
applications as a
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Seguence 19 AA;

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100.0%; Score 78; DB 2; Length 19; 100.0%; Pred. No. 2.6e-06; ive 0; Mismatches 0; Indels
    100.0%; Fr.
100.0%; Fr.
                                                             1 TPDINPAWYAGRG 13
                                13; Conservative
                 Best Local Similarity
    Query Match
                                Matches
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Gaps

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AAW95185 standard; peptide; 19 AA. 10-MAR-1999 AAW95185; 

Bovine pituitary-derived ligand polypeptide partial sequence. (first entry)

Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.

Bos sp.

WO9849295-A1

05-NOV-1998,

98WO-JP001923, 27-APR-1998; 97JP-00109974.

(TAKE ) TAKEDA CHEM IND LTD.

Fukusumi S; Hinuma S,

WPI; 1999-009423/01.

polypeptide ligand for orphan G protein coupled receptors - used for ating disorders of central nervous system, pituitary and pancreas, and Example 16; Page 145; 206pp; English. treating disorders for drug screening

The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or URR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically,

The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention

Sequence 19 AA;

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e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases. Acteutzeld-dakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis, epilepsy and many others; also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of polypeptide DNA is used as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisers, in drug development; for gene therapy and to develop transgenic animals. The present sequence represents a bovine pituitary derived ligand polypeptide obtained by N-terminal sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific_cleavage sites.
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide production by gene recombination associated peptide #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide production; low-molecular peptide; KiSS-1; GFR8 ligand; gene recombination.
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                                                                                                                                                                                                                                                              100.0%; Score 78; DB 2; Length 19; 100.0%; Pred. No. 2.6e-06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 60; 87pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU60830 standard; peptide; 19 AA.
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                                                                                                                                                                                                                                                                                                 13; Conservative
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                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                  Sequence 19 AA;
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ABU60830
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Gaps

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Indels

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Mismatches

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13; Conservative

Matches

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This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 34 to 53 of the sequence in AMN3186 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone consciousness, anxiety syndrome, schizophrolactinaemia, diabetes, hyperglyceridaemia, hyperlipdaemia, hyperfolactinaemia, diabetes, cancer, pancreatitis, spinal disease, Turner's syndrome, neurosis, cancer, pancreatitis, spinal injury, transient brain ischaemia, amylotrophic lateral sclerosis, acute myocardial infarction, camplorosis, asthma, epilepsy, infertility and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering to binding activity of the ligand thus affecting activation of the G protein-coupled receptor protein
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                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor; ligand binding; pharmaceutical; modulator;
pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujii R, Fukusumi S;
                                 ö
                                                                                                                                                                                                                                                                                             Bovine G protein-coupled receptor ligand peptide fragment 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 78; DB 2; Length 20; Pred. No. 2.8e-06;
 Length 19;
                                 0; Indels
Score 78; DB 6; I
Pred. No. 2.6e-06;
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                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 161; 258pp; English.
                                                                                                                                                                                             AAW31374 standard; peptide; 20 AA.
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95JP-00059419.
96JP-00211805.
Query Match
Best Local Similarity 100.0%;
Matches 13; Conservative 0;
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                                                                                                                                                                                                                                                                  (first entry)
                                                                      1 TPDINPAWYAGRG 13
                                                                                                       TPDINPAWYAGRG 13
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N-PSDB; AAV02397.
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15-MAR-1996;
12-AUG-1996;
18-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hinuma S,
Kitada C;
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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated complets a ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other cissues and cam be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, c.g. to treat senile dementia, Alzheimer's, Parkinson's or Huntington's disabetes; schizophrenia; disorders of growth hormone secretion; cancer; cheumatodia entiritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgent animals carrying the ligand polypeptide encoding DNA or its muteain animals cutypeptide DNA is used as a source of probes and primers; to identify of polypeptide DNA is used as a source of probes and primers; to identify crelated sequences; in receptor-binding assays; for production of Ab and animals. The present sequence represents a bovine genome-derived ligand polypeptide fragment which is similar to the murine ligand-polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening.
                                                                                                                                                                                                                                                                            pitultary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pitultary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; huntington's disease; drug; cretizfeld-Jakob disease; posoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.
                                                                                                                                                                                                                                         Bovine pituitary-derived ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 19; Page 151; 206pp; English.
                                                                                                                                   A.
                                                                                                                                   AAW95191 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-00109974.
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1 TPDINPAWYAGRG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-009423/01.
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                                                                                                                  AAW95191
                                                                                                RESULT
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Length 20;

2 ; DB

Score 78;

100.08;

Query Match

100.0%; 100.0%;

Query Match Best Local Similarity

0,

Gaps

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Indels

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Mismatches

.. 0

13; Conservative

Matches

1 TPDINPAWYAGRG 13

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1 TPDINPAWYAGRG

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The present sequence represents a bovine pituitary-derived ligand fragment: It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for reating or preventing hypometabolism. However, cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting actation in a demestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing prolaction can be used for treating or preventing prolactions. Drain thumour, emmeniopathy, autoimmune disease, prolactinoma, infertility, impotence, amenorthaa, galactorrhea, prolactinoma, infertility, impotence, amenorthaa, galactorrhea, coromegaly, Chiari-Frommel Syndrome, Argonz-del Castilo syndrome, Porbestonibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthirity fetus, abnormal saccharometabolism, abnormal lipidametabolism or oxytocia
                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor; GPCR; hypcovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                         prolactinoma; infertility; impotence; amenorhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Frobses-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                          Bovine pituitary-derived ligand; modulation; prolactin secretion;
                                 .,
                               0; Indels
                                                                                                                                                                                                                                                                                                                        Bovine pituitary-derived ligand polypeptide fragment.
            Pred. No. 2.8e-06;
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100.0%; Prec. ....
                                                                                                                                                                                                    AAW97232 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-JP002765
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                                                                1 TPDINPAWYAGRG 13
                                                                                                        TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                     (first entry)
      Similarity 100.
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                                                                                                                                                                                                                                             AAW97232;
      Best Local
Matches 1
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Monoclonal antibody, 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic.

19P2 ligand peptide fragment.

(first entry)

22-FEB-2000

AAY49301;

AAY49301 standard, peptide; 20 AA.

RESULT 7 AAY49301 20 /note= "C-terminal amide"

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Kitada C, Hinuma

Matsumoto H,

WPI; 2000-039381/03.

(TAKE ) TAKEDA CHEM IND LID,

99WO-JP002650 98JP-00140293

20-MAY-1999; 21-MAY-1998;

Location/Qualifiers

Key Modified-site

Bos sp.

409960112-A1

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                                                                                                                                                                                                                                                                                                                                                                                               New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 19P2 ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 100.0%; Score 78; DB 3; Length 20 I Similarity 100.0%; Pred. No. 2.8e-06; 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 27, 73pp, Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB10350 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 AA;
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Score 78; DB 2; Length 20; Pred. No. 2.8e-06;

100.0%;

Query Match Best Local Similarity Sequence 20 AA;

17-MAY-2000; 2000WO-US013576.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a bovine peptide which acts as an oxytocin secretion
                                                Bovine; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                   Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl, maleimido group, amino, hydroxyl; thiol; hormone, growth factor, neurotransmitter.
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                 Bovine oxytocin secretion promoting peptide SEQ ID NO: 6.
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                                                                                                                                                                                                                                                                                                                                    Matsumoto H, Kitada C, Hinuma S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 51; 72pp; Japanese.
                                                                                                                                                                                                                                   99WO-JP007199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
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                                                                                                                                                                 WO200038704-A1.
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                                                                                                                                                                                                                                                                   25-DEC-1998;
                                                                                                                                                                                                                                   22-DEC-1999;
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                                                                                                                                                                                                   06-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB90996;
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The present invention describes a modified therapeutic peptide (I)

comprising a therapeutically active amino acid region (III) and a
reactive group (II) (e.g. succinimidy! and malemido groups) attached
to a less therapeutically active amino acid region (IV), which covalently
bonds with amino/hydroxy//thiol groups on blood components to form a
peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth
factors and neurotransmitters, to protect them from peptidase activity in
vivo for the treatment of various disorders. Bndogenous therapeutic
peptides are not suitable as drug candidates as they require frequent
administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or
reduces the action of peptidases to increase length of activity (half
life) and specificity as bonding to large molecules decreases
ABB90829 to AAB93441 represent peptides which can be used in the
exemplification of the present invention
                                                                                                                                                                                                         Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPR10; UHR-1; PTRP receptor; prolactin-releasing peptide; pain; central nervous system disorder; autonomic regulation; analgesic;
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                                                                                                                                      Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 78; DB 4; Length 20 Best Local Similarity 100.0%; Pred. No. 2.8e-06; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                      Ezrin AM, Milner PG, Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminal amide"
                                                                                                                                                                                                                                                         Disclosure, Page 245; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB46954 standard; protein; 20 AA.
                               99US-0134406P.
99US-0153406P.
99US-0159783P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000; 2000WO-F1000664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00365756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypotensive; blood pressure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide PrRP20 fragment
                                                                                                    (CONJ-) CONJUCHEM INC.
                                                                                                                                                                       WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 AA;
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1999;
                               17-MAY-1999;
10-SEP-1999;
                                                                 15-OCT-1999;
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                                                                                                                                    Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB46954;
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20-MAR-2000; 2000US-00531567.

Matsumoto H, Hinuma

Kitada C,

Korpi

(TAKE ) TAKEDA CHEM IND LTD.

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This invention describes a novel C-terminal fragment (I) of an isolated CC prolactin-releasing peptide (PRRP), referred to as PrRP20 and having a sequence (S1). The invention also describes (I) a therapeutic composition (C1) comprising (I) or a C-terminal fragment of PRRP referred to as PRRPB and comprising (I) or a C-terminal fragment of PRRP referred to as PRRPB against PRRP20 for identification of disorders involving the central regulation, where specific antisera against the N-and/or C-terminal commins of PRRP is used to identify alterations in PRRP synthesis or regulation, where specific antisera against the N-and/or C-terminal commins of PRRP is used to identify alterations in PRRP synthesis or levels; (I) a rat or human receptor encoded by a 1122 nucleotide sequence (S3), fully defined in the specification; (4) treating a person suffering from a disorder regulated by a receptor (II) encoded by a sequence of 1122 nucleotide sequence. (II) when a gonist or antagonist to the central nervous system, by administering an agonist or antagonist to the receptor; and (5) treating blood pressure, by blocking of receptors of PRRP or its C-terminal fragment G1y10ArgProvalG1yArgPhe-NH 2 (S2). (The products of the invention have analgesic and hypotensive activity. (C1) is useful for regulating bain, for manufacturing a medicament for regulating blood pressure, and for treating pain. Agonist and antagonist of (II) are useful for treating action one to pain, inflammatory committed in the blood pressure.
                                                                                                                                                             prolactin-releasing peptide useful for regulating in the manufacture of a medicament for regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cow; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 78; DB 4; Length 20; 100.0%; Pred. No. 2.8e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine CRH releasing protein related peptide SEQ ID NO: 6.
                                                                               Pertovaara A, Kalso E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG62519 standard; peptide; 20 AA.
                                                                                                                                                                                                                                     Claim 1; Page 10; 40pp; English.
                                     (JUVA-) JUVANTIA PHARMA LTD OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-NOV-1999; 99JP-00327900.
26-SEP-2000; 2000JP-00297073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                         C-terminal fragments of autonomic functions and
                                                                                                                   WPI; 2001-182941/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 AA;
                                                                                                                                                                                                   blood pressure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200135984-A1.
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AAG62519
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Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion.
                                                                                                                                                                         The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor ligand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nauses, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wakefulness; sleep disorder; prolactin releasing peptide receptor; PrRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea; insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 78; DB 4; Length 20; 100.0%; Pred. No. 2.8e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine PrRP-31 C-terminal peptide, PrRP-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE26402 standard; peptide; 20 AA.
                                                                                                                                                 Claim 4; Page 64; 90pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .7-AUG-2001; 2001US-00932161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                          13; Conservative
                                                                         WPI; 2001-355552/37
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                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CIVE/) CIVELLI O.
                                                                                                                                                                                                                                                                                                                                              Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE26402;
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Disclosure, Page 24; 35pp; English.

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The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a proladcin releasing peptide (PrRP) receptor (GPRIO) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. The preceptor agonists may be used to treat common disorders which lead to sleepiness, e.g. sleep appose, narcolepsy, idiopathic hypersomnia and psychogenic hypersomnia. PrRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep disorder and psychophysiologic insomnia. The present sequence is bovine PRRP-31 C-terminal peptide, PRRP-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a trarget peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide production by gene recombination associated peptide #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          production; low-molecular peptide; KiSS-1; GPR8 ligand;
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 78; DB 5; Length 20; 100.0%; Pred. No. 2.8e-06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 62; 87pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU60834 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAY-2002; 2002WO-JP004735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001; 2001JP-00147341.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-129302/12.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene recombination
                                                                                                                                                                                                                                                                                                                          Sequence 20 AA;
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This sequence represents a peptide fragment of a novel bovine pituitary derived ligand corresponding to amino acid residues 34 to 54 of the sequence in Amalis68 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper and polyphagia, hypercholesterolaemia, consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper and polyphagia, hypercholesterolaemia, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, remental cancer is propolated atthritis, spinal injury, transient brain ischaemia, amylotrophic lateral sclerosis, acute myocardial infarction, anylotrophic lateral sclerosis, acute myocardial infarction, spinal asthma, epilepsy, infertility and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering containing activity of the ligand thus affecting activation of the G
                                  ö
                                                                                                                                                                                                                                                                                                           protein-coupled receptor; ligand binding; pharmaceutical; modulator; tuitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ligand peptide for G protein-coupled receptor - acts by modulating function in the central nervous system, pancreas and pituitary gland.
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fukusumi S;
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O
                                                                                                                                                                                                                                                                            Bovine G protein-coupled receptor ligand peptide fragment 5.
Length 20;
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujii R,
 Score 78; DB 6; Li
Pred. No. 2.8e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hosoya M,
                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 162; 258pp; English.
                                                                                                                                                                               AAW31375 standard; peptide; 21 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95JP-00343371.
96JP-00059419.
96JP-00211805.
96JP-00246573.
 100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                06-APR-1998 (first entry)
                                                                                           1 TPDINPAWYAGRG 13
                                                                 1 TPDINPAWYAGRG 13
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N-PSDB; AAV02398.
                  Similarity
                                                                                                                                                                                                                                                                                                                                               therapeutic agent.
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12-AUG-1996;
18-SEP-1996;
     Query Match
Best Local Simil
Matches 13;
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                                                                                                                                                                                                                                                                                                                                                                                30s taurus.
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Kitada C;
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Length 21;

DB 2;

Score 78;

100.08;

Query Match

Sequence 20 AA;

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The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated G Philo (human) or URI». (rat). Calls transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases, Creutzfeld-Jakob disease, poisoning by heavy metals or drugs; contained arthritis, epilepsy and many others, also to improve post-coperative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to struction of the polypeptide expressing genes, as models of struction of the polypeptide expressing genes, as models of struction of the polypeptide expressing genes, as models of struction of the polypeptide expressing genes; as models of struction of the polypeptide expressing genes; and models of struction of the polypeptide seques; for production of Ab and antisers, in drug development; for gene therapy and to develop transgenic antisers, in drug development; for gene therapy and to develop transgenic antisers, in drug development; is similar to the murine ligand-polypeptide
                                                                                                                                                                                                                                                                                                                                                                              Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor; GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer; disease; Parkinson's disease; Huntington's disease; drug; Creurzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide ligand for orphan G protein coupled receptors - used for treating disorders of central nervous system, pituitary and pancreas, and for drug screening.
                             Gaps
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                                                                                                                                                                                                                                                                                                                                        Bovine pituitary-derived ligand polypeptide fragment
    100.0%; Pred. No. 2.9e-06; tive 0; Mismatches 0;
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                                                                                           (first entry)
                                                                  1 TPDINPAWYAGRG 13
Best Local Similarity 100.
Matches 13; Conservative
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Sequence 21 AA;

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    Length 21;
Query Match 100.0%; Score 78; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 13; Conservative 0; Mismatches 0;
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Job time : 28.7122 secs
                                                                               1 TPDINPAWYAGRG 13
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Sequence 82, Appl Sequence 84, Appl Sequence 86, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 14, Appl Sequence 14, Appl Sequence 1, Appl Sequence 18, Appl Sequence 18, Appl Sequence 15, Appl Sequence 6127, Appl Sequence 6127, Appl Sequence 6127, Appl Sequence 218693, Sequence 218693, Sequence 218693, Sequence 74, Appl Sequence 50882, Appl Sequence 50882, Appl Sequence 518693, Sequence 2170, Appl Sequence 50882, Appl Sequence 50882, Appl Sequence 51863, Appl

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Sequence 27, Application US/10044592;
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: FIREMENTION:
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: US/10/094,592
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1999-26-10
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NOS: 96
13 US-10-044-592-82
13 US-10-044-592-84
13 US-10-044-592-86
13 US-10-044-592-86
13 US-10-044-592-86
14 US-10-064-592-6
15 US-09-932-161-17
17 US-10-064-592-4
18 US-10-06-777-17
19 US-10-044-592-4
19 US-10-044-592-94
2 US-10-044-592-94
2 US-10-044-592-94
3 US-10-044-592-94
19 US-10-044-592-95
2 US-10-26-777-15
2 US-10-26-777-15
2 US-10-26-777-15
2 US-10-26-777-15
3 US-10-36-493-6327
5 US-10-26-963-197
5 US-10-26-068-74
10 US-10-28-963-19893
10 US-10-374-780A-356
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Best Local Similarity 100.0%; Pred. No. 2.1e-05; Matches 13; Conservative 0; Mismatches 0;
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US-09-392-161-16
is agenence 16, Application US/09932161
Parent No. US20020037533A1
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          ORGANISM: Bovine
US-10-044-592-27
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TYPE: PRT
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                                                                                                                        (without alignments)
177.617 Million cell updates/sec
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Sequence 28,
Sequence 38,
                                                                                                        August 12, 2004, 14:49:10 ; Search time 22.9767 Seconds
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| cgn2_6/ptodata/2/pubpaa/PCT_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_PME_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_PME_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-932-161-16

US-09-932-161-16

US-10-096-7-77-16

US-10-044-592-43

US-10-044-592-26

US-10-044-592-26

US-09-932-161-13

US-09-932-161-13

US-09-932-161-13

US-09-932-161-13

US-09-932-161-13

US-10-044-592-39

US-10-044-592-41

US-10-044-592-41

US-10-044-592-81

US-10-044-592-81

US-10-044-592-81

US-10-044-592-81

US-10-044-592-81
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                                                                                                                                                                                                                                                        1292805 seqs, 313927144 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Publication No. US20030171270A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating TO Prolactin Releasing Peptide (PRRP)
FILE REFERENCE: P-UC 534
CURRENT APPLICATION UMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
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US-10-044-592-42

Sequence 42, Application US/10044592

Publication No. US2020143152A1

SERNERAL INFORMATION:
APPLICANT: Hinuma, Shuji

APPLICANT: Hinuma, Shuji

ITILE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P

CURRENT FAPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: US 09/403639

PRIOR APPLICATION NUMBER: US 09/403639

PRIOR APPLICATION NUMBER: US 9-109974

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-28

NUMBER OF SEQ ID NOS: 96
                                 APPLICANT: Lin, Seven
TITLE OF INVENTION: Screening and Therapeutic Methods For ITLE OF INVENTION: Screening and Therapeutic Methods For ITLE OF INVENTION: Promoting Wakefulness and Sleep FILE REPERENCE: P-UC 46'99
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR PILING DATE: 2000-04-28
NUMBER OF SEC ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
ILENGTH: 20
TYPE: PRT
CRGANISM: Bos taurus
US-09-932-161-16
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Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels
                       APPLICANT: Civelli, Olivier
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GENERAL INFORMATION:
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LENGTH: 20
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US-10-044-592-43

Sequence 43, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinima, Shuji

TITLE OF INVENTION: Shoji

TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 1999-25-10

PRIOR FILING DATE: 1999-25-10

PRIOR FILING DATE: 1998-04-27

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SOFFWARE:

SOFFWARE:
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APPLICANT: Fukusumi, Shoji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REPERCORS: 46530SP
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT PILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: POT/JD98/01923
PRIOR APPLICATION NUMBER: PT/JD98/01923
PRIOR APPLICATION NUMBER: PP-10974
PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
                                                                                                                                                                                                                        Length 20;
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100.0%; Score 78; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 13; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US/09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SEQTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 20
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Sequence 44, Application US/10044592;
Publication No. US20020143152A1;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       1 TPDINPAWYAGRG 13
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                                                                                                                              TYPE: PRT

ORGANISM: Bos taurus
US-10-096-777-16
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Matches 13; Conserv
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LENGTH: 21
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Sequence 39, Application US/10044592

Sequence 39, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
ITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 2002-01-10
PRIOR FILING DATE: 2908-01-10
PRIOR FILING DATE: 1998-25-10

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1999-04-28

NUMBER: OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                       US-09-932-161-13
Sequence 13, Application US/09932161
Sequence 13, Application US/09932161
Sequence 13, Application US/09932161
Sequence 13, Application US/09032161
Sequence 13, Application US/09032161
APPLICANT: Civelli, Olivier
APPLICANT: Civelli, Olivier
TITLE OF INVENTION: Screening and Therapeutic Methods For INTER OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERRING: Promoting Wakefulness and Sleep
CURENT APPLICATION NUMBER: US/09/932,161
CURENT APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 131
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                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 13; Conservative 0; Mismatches 0;
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                                                                                                                                                Score 78; DB 13;
Pred. No. 3.1e-05;
                                                                                                                                                                                           0; Mismatches
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Best Local Similarity 100.0%;
Matches 13; Conservative 0
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US-09-932-161-13
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US-10-044-592-39
                                                           TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-26
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SEQ ID NO 39
LENGTH: 31
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                  SEQ ID NO 26
LENGTH: 29
SOFTWARE
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                                                                                                                                                                                                                                                                                                                                           Sequence 78, Application US/10044592

Sequence 78, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinnuma, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use

TITLE REFRENCE: 2464USEP;

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT APPLICATION NUMBER: US/10/044,592

PRIOR FILING DATE: 1998-01-10

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE:

SEQ ID NO 78

LENGTH: 25

TYPE: PRI
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US-10-044-592-26
Sequence 26, Application US/10044592
Sequence 26, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICAMT: Hinuma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REPERENT SPOINTS: 2663USEP;
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT PILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1939-25-10
PRIOR FILING DATE: 1939-05-10
PRIOR PILING DATE: 1939-05-10
PRIOR FILING DATE: 1939-05-10
PRIOR FILING DATE: 1939-05-10
PRIOR FILING DATE: 1939-04-27
NUMBER OF SEQ ID NOS: 96
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                                                                                                             100.0%; Score 78; DB 13; Length 22; 100.0%; Pred. No. 2.4e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
| LOCATION: (1)...(20)
| COTHER INFORMATION: primer
| NAME/KEY: misc_feature
| LOCATION: (52)...(76)
| COTHER INFORMATION: primer
US-10-044-592-78
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Best Local Similarity 100.
Matches 13; Conservative
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       LENGTH: 22
TYPE: PRT
CORGANISM: Bovine
US-10-044-592-44
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US-10-044-592-78
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APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: PolyPeptides, their Production and Use
FILE REPERENCE: 2453US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1099-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 41
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 78; DB 13;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 13; Conservative 0; Mismatches 0;
                                                                       Sequence 41, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 13; Conservative
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                             RESULT 13
US-10-044-592-41
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                                                 Gaps
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APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating TO Prolactin Releasing Peptide (PRRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
PRIOR APPLICATION NUMBER: US/09/560,915
PRIOR FILING DATE: 2000-03-12
PRIOR FILING DATE: 2000-04-28
SUFFWARE: FASTERO FOR Mindows Version 4.0
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US-10-044-592-40

is Sequence 40, Application US/10044592

is Publication No. US20020143152A1

is GENERAL INFORMATION:

is APPLICANT: Hinuma, Shuji

is APPLICANT: Hinuma, Shuji

is TITLE OF INVENTION: Polypeptides, their Production and Use

ITILE OF INVENTION: Polypeptides, their Production and Use

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT APPLICATION NUMBER: US 09/403639

is PRIOR APPLICATION NUMBER: US 09/403639

PRIOR FILING DATE: 1998-02-10

is PRIOR APPLICATION NUMBER: DY 9-109974

PRIOR FILING DATE: 1998-04-27

is NUMBER OF SEQ ID NOS: 96

is SOFTWARE:

is SEQ ID NO 40

is ERWITH: 32

is NUMBER OF SEQ ID NOS: 96

is ERWITH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%; Score 78; DB 14; Length 31; 1 Similarity 100.0%; Pred. No. 3.3e-05; 13; Conservative 0; Mismatches 0; Indels
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                   Pred. No. 3.3e-05;
; Mismatches 0; Indels
                                                                                                                                                                                                                       US-10-096-777-13
Sequence 13. Application US/10096777
Publication No. US20030171270A1
GENERAL INFORMATION:
100.0%; Pre-
                                                                                     1 TPDINPAWYAGRG 13
                                                                                                                   Best Local Similarity 100.
Matches 13; Conservative
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ORGANISM: Bos taurus
US-10-096-777-13
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Matches 13; Conserv
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; ORGANISM: Bovine
US-10-044-592-40
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Indels

Length 33;

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Gaps
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Sequence 28, Application US/10044592;
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Pukusumi, Shoji
ITLE OF INVENTION: Polypeptides, their Production and Use;
FILE REFRENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT APPLICATION NUMBER: US/09/403639
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1998-25-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1998-25-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR PLING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: UP 9-109974
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 96
LENGTH: 98
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Sequence 38, Application US/100
Publication No. US20020143152A1
GENERAL INFORMATION:
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12 TPDINPAWYAGRG 24

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## APPLICANT: Hinuma, Shuji
## APPLICANT: Fukusumi, Shoji
## TITLE OF INTENTION: PolyPeptides, their Production and Use
## TITLE OF INTENTION: PolyPeptides, their Production and Use
## TITLE OF INTENTION: PolyPeptides, their Production and Use
## CURRENT APPLICATION NUMBER: US/10/044,592
## CURRENT FILING DATE: 1939-25-10
## PRIOR FILING DATE: 1939-25-10
## PRIOR FILING DATE: 1939-42-7
## PRIOR FILING DATE: 1999-04-27
## PRIOR FILING DATE: 1997-04-28
## PRIOR FILING DATE: 1997-04-28
## PRIOR FILING DATE: 1997-04-28
## PRIOR PILING DATE: 1997-04-28
## PRIOR FILING DATE: 1997-04-28
## PRIOR FILING DATE: 1997-04-28
## PRIOR FILING DATE: 1997-04-28
## PRIOR PILING DATE: 1997-04-29
## PRIOR PILING DATE: 1999-04-29
## PRIO
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33, Appl
122, Appl
122, App
131, App
136, App
40, Appl
50, Appl
41, Appl
41, Appl
51, Appl
51, Appl
52, Appl
52, Appl
52, Appl
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Suenaga, Masato
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Mishimura, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
WUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plop MS-DOS
COREMARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
PRILING DATE: 26-UN-1998
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: COALIN, DAVIA G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-52-3400
                                US-09-421-208-33
US-08-776-971-1
US-08-776-971-124
US-08-776-971-132
US-08-776-971-131
US-08-776-971-136
US-08-776-971-136
US-09-776-971-50
US-09-560-915-17
US-09-560-915-17
US-09-560-915-17
US-09-560-915-17
US-09-776-971-50
US-09-421-208-32
US-09-105-678A-33
US-08-776-971-7
                                                                                                                                                                                 US-09-421-208-41
US-09-105-678A-42
US-08-776-971-52
                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                       ; Sequence 30, Application US/09105678A; Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 19 amino acids
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 130 W
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COUNTRY: US/
ZIP: 02109
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US-09-105-678A-30
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Sequence 29, Appli
Sequence 31, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 33, Appli
Sequence 33, Appli
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App
Appl
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                                                                                       August 12, 2004, 14:37:36 ; Search time 7.40698 Seconds (without alignments) 90.609 Million cell updates/sec
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Sequence 98,
Sequence 34,
Sequence 16,
Sequence 35,
Sequence 9, A
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. /cgn2_6/ptodata2/iaa/5A_COMB.pep:*
. /cgn2_6/ptodata2/iaa/5B_COMB.pep:*
. /cgn2_6/ptodata3/iaa/6A_COMB.pep:*
. /cgn2_6/ptodata3/iaa/6B_COMB.pep:*
. /cgn2_6/ptodata2/iaa/BE_COMB.pep:*
. /cgn2_6/ptodata3/iaa/PCTUS_COMB.pep:*
. /cgn2_6/ptodata3/iaa/PCTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-105-678A-30
US-08-76-971-4
US-09-421-208-34
US-09-105-678A-34
US-09-105-678A-34
US-09-105-678A-31
US-09-105-678A-31
US-09-105-678A-31
US-08-776-971-9
US-09-105-678A-31
US-08-776-971-11
US-08-776-971-11
US-08-776-971-11
US-09-105-678A-31
                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                            389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    protein search, using sw model
                                                                                                                                         US-09-700-643A-1_COPY_12_24
                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000.00
1000.00
1000.00
1000.00
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                                                                                                                                                       Perfect score:
                                                                                                                                                                                           Scoring table:
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Maximum DB
                                                                     OM protein
                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
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1 TPDINPAWYAGRG 13

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Kawmera, Yuji
Hosoya, Masaki
Fujii, Ryo
Fujii, Ryo
Fukumi, Shoji
Kitada, Chieko
TITLE OF INVENITON: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LIP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 78; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM INTERCOMPALIBLE
COMPUTER: IBM COMPALIBLE
CORRENT G SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
PILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIPICATION: cullature.

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP /343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: JF 8/21805
ATTORNEY/ACENT INFORMATION:
NAME: CONIN, DAVIG G.
REGISTRATION NUMBER: 47176
TELECOMMUNICATION NUMBER: 47176
TELECOMMUNICATION NUMBER: 47176
TELECOMMUNICATION NUMBER: 47176
TELEFAX: 617-523-5440
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein FRAGNENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 4
Sequence 4, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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Gaps
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                                  GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 19;
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APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                        CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parent: Pc-mpatible
OPERATING SYSTEM: Pc-mps/ms-nps/
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 78; DB 3;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 13; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
Sequence 30, Application US/09421208
Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34, Application US/09105678A Patent No. 6103882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27,026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Conlin, David G.
REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / NOLECULE TYPE: peptide US-09-421-208-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-105-678A-34
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RESULT 3

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APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
                              APPLICATION NUMBER: JP 8/211805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 98, Application US/08776971B; Patent No. 6228984; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPDINPAWYAGRG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Habata
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Matches 13; Conserv
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US-08-776-971-98
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Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 78; DB 3; Length 20; 100.0%; Pred. No. 8.4e-07; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC COMPATIBL
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: UP 172118/1997
FILING DATE: 77-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAMM: COMIN, DATA:
REGISTRATION NUMBER: 48466-342
FILECOMMUNICATION INFORMATION:
TELEBRACE/DOCKET NUMBER: 48466-342
TELEBRACE/DOCKET NUMBER: 48466-342
TELEBRACE/DOCKET NUMBER: 48466-342
TELEBRACE/DOCKET NUMBER: 3400
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <10kmovm>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/JD96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULY:
US-08-776-971-8
US-08-776-971-8
Sequence 8, Application US/08776971B
Fatent No. 6228984
GENERAL INFORMATION:
Habata, Yugo
Kawamata, Yujo
Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-105-678A-34
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Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 100.0%; Score 78; DB 3; Length 20; Il Similarity 100.0%; Pred. No. 8.4e-07; 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNknown>
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-ESP-196
ATTORNEY/AGBUT INFORMATION:
NAME: CONIIN, David G.
REGIGSTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-776-971-8
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Gaps
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                      0; Indels
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APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
MUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
1: 130 Water Street
Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FLING APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FLING APPLICATION TOWN PROBLEMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 78; DB 4; I 100.0%; Pred. No. 8.4e-07;
                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-09-105-678A-35
Sequence 35, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
                                                                                                                                                                      US-09-560-915-16
; Sequence 16, Application US/09560915
; Patent No. 6383764
                    ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
                                                        1 TPDINPAWYAGRG 13
                                                                                           1 TPDINPAWYAGRG 13
                    13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TPDINPAWYAGRG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
COUNTRY: US!
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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CITY: BO
                Matches
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Best Local Similarity 100.0%; Score 78; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 78; DB 3; Length 20; Pred. No. 8.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osomu
IITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHWAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALUMESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REPERENCE/DOCKET NUMBER: 47176
TELEPONMUNICATION INFORMATION:
TELEPAS: 617-523-3400
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 mino acids
TYPE: anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: anino acids
                                                                                                                                                                                                                       ; TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 98: US-08-776-971-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1997
FILING DATE: 27-UN-1997
FILING DATE: 27-UN-1997
ATTORNEY CONLIN, DAVIG G.
REGISTATION NUMBER: 27,026
REFERENCE/OCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34, Application US/09421208
Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                        1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / MOLECULE TYPE: peptide
US-09-421-208-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:

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Gaps
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                                                                                                                                                                                                                                                                                              Sequence 35, Application US/09421208

Patent No. 6258561

GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
ITTLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street

CITY: Boston
                                                              Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OURREATING SYSTEM: C-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION NUMBER: US 09/105,678
FILING DATE: 2-JUN-1998
APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1998
APPLICATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-3400
TELEPHONE: G17-523-3400
TELEPHONE: G17-523-3400
TELEPHONE: G17-523-3400
TELEPHONE: G17-523-5440
                                                          Query Match
100.0%; Score 78; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
; SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-08-776-971-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-105-678A-36
; Sequence 36, Application US/09105678A
; Patent No. 6103882
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ilarity 100.0%;
Conservative 0,
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYAGRG 13
                                                                                                                                                       1 TPDINPAWYAGRG 13
                                                                                                                                                                                                 1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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USA
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Sequence 9, Application US/08776971B
Sequence 9, Application US/08776971B
Patent No. 6228994
GENERAL INFORMATION: Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
                                                                                                                                                                         ch 100.0%; Score 78; DB 3; Length 21; al Similarity 100.0%; Pred. No. 8.9e-07; 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN,
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: O6-Feb-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION SCHLAUDWILL
PRIOR APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28 -DC-1996
APPLICATION NUMBER: JF 7/343371
FILING DATE: 28 -DC-1995
APPLICATION NUMBER: JF 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JF 8/211805
FILING DATE: 12-A01996
APPLICATION NUMBER: JF 8/246573
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
      SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                           1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                   1 TPDINPAWYAGRG 13
                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
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US-08-776-971-9
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100.0%; Score 78; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Stenage, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Mashimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: CURKNOWN>
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APPLICATION NUMBER: US/09/421,208
                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DT /343371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: COALIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-776-971-10
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APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-421-208-36
; Sequence 36, Application US/09421208
; Patent No. 6258561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TPDINPAWYAGRG 13
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Posya, Masaki
Fusii, Ryo
Fukusumi, Shoji
Xitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 22;
                  APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                       ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                     COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
ATHOR APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 9
Matches 13; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-09-105-678A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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Patent No. 6228984

GENERAL INFORMATION

FABDATA, YUGO

FURNAMATIA, YUGO

FURNSAMIA, YUJI

FORDI, RYO

FURNSAMI, RYO

FURNSAMI, RYO

TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE

NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIEG, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 110 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 78; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MASCON
STATE: MASCON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: ISM compatible
COMPUTER: ISM compatible
SOFTWARE: FASIENCE for Windows Version 2.0
SOFTWARE: FOR SASIENCE for Windows Version 2.0
FILING DATE: 06-Feb.1997
APPLICATION NUMBER: UP 9/3371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: UP 8/246573
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: UP 8/246573
ATPORNEY AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
RESERRANCE/DOCKET NUMBER: 47176
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGRAT INFORMATION:
NAME: COLLIN, DAVIG G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEFRAM: 617-523-340
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERSISTICS:
LENGTH: 22 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TPDINPAWYAGRG 13
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-421-208-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                                                                             TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-776-971-111
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August 12, 2004, 14:37:36; Search time 5.74419 Seconds (without alignments) 217.697 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                          283366 segs, 96191526 residues
                                                                                                                                                                                     US-09-700-643A-2_COPY_12_24
76
1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *
                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote probable polyketid	probable polyketid	elastic titin - hu	bacterioferritin c	nitrite extrusion	probable glucose t	probable sugar tra	ATP-dependent heli	probable 1-acylgly	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	phosphoglycerate m	probable peptidase
T21432 T03222	T03223	I38346	G75424	C83160	T05156	E81287	E75523	D64688	T05418	A97505	AE2723	B72686	AH1944	T35304
01 02	7	N	7	~	~	~	C)	7	~	N	7	~	(7	(4)
1711	2100	7962	163	468	508	612	822	240	352	105	105	118	212	282
52.6	52.6	52.6	51.3	51.3	51.3	51.3	51.3	50.7	50.7	50.0	50.0	50.0	50.0	50.0
0 4 0 0	40	40	39	39	39	39	39	ω	38.5			38		38
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1	
UC/80/ prolactin-releasing peptide - rat Cr.Species: Rattus norvegicus (Norway rat) C.Date: 30-Jun-2001 #sequence revision 30-Jun-2001	s - rat 1s (Norway rat) nce revision 30-Jun-2001 #text_change 30-Jun-2001
C, Accession: JC7607 R, Yamada, M., Ozawa, A., Ishii,	- shii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T
Blochem. Blophys. Res. Commun. A;Title: Isolation and characte A;Reference number: JC7607; MU	Blochem. Blophys. Res. Commun. 2841, 53-56, 2001 AjTitle: Isolation and characterization of AjReference number: JC7607; WUID:21092785; PMID:11178959
A; Contents: Spleen A; Accession: UC7607 A; Molecule type: DNA A: Deciding: 1-82 vana	
A.Cross-references: DDBJ:AB040612; DDBJ:AB040613 C.Comment: This peptide induces arachidonic acid	A.Cross-references: DDBJ.AB040612; DDBJ.AB040613 A.Cross-references: DDBJ.AB040612; DDBJ.AB040613 A.Cross-references: Dispeptive induces arachidonic acid metabolite release from rat anterior problems and primilation of arms experion from the nithiany
C, Genetics: A, Gene : PTRP A, Introns: 33/1	
Query Match Best Local Similarity 84.66 Matches 11; Conservative	89.5%; Score 68; DB 2; Length 83; 84.6%; Pred. No. 0.00022; .ive 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TPDINPAWYASRG 13	
Db 33 TPDINPAWYIGRG 45	
RESULT 2	
hypothetical protein F38E11.7 - C. C;Species: Caenorhabditis elegans	1.7 - Caenorhabditis elegans Slegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_ C;Accession: T21969	nce_revision 15-Oct-1999 #text_change 15-Oct-1999
R;Matthews, P. submitted to the EMBL Data Lib) A:Reference number: Z19495	Library, January 1996
A, Accession: T21969	דיחתה/ זחעה/ היים ביים ביים ביים
A;Status: preliminary; translated from GS/EMBL/DDBD A;Molecule type: DNA	nBlated from GB/EMBL/DDBO
A; Kesidues: 1-70/ Anily A; Cross-references: EMBL: Z6834; A; Experimental source: clone F'	A.Kosluudes: 1-70, XMIL.) A.Gross-references: EMB:268342; PIDN:CAA92775.1; GSPDB:GN00022; CESP:F38E11.7 A.Experimental source: clone F38E11
C;Genetics: A;Gene: CESP:F38E11.7 A:Map position: 4	
118/1;	139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1;
Query Match Best Local Similarity 75.0	59.2%; Score 45; DB 2; Length 767; 75.0%; Pred. No. 16;

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Gaps

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conserved hypothetical protein PA2151 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15.Sep-2000 #sequence_revision 15.Sep-2000 #text_change 31-Dec-2000 C;Accession: F83376 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoy A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: F83376
A/Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related to BCS1 protein precursor [imported] - Neurospora crassa
NyAlternate names: protein B23L21.300
Syspecies: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49717
Syschulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
                                     C,Accession: T10236
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes, submitted to the Protein Sequence Database, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: ATSP:TIIII1.140
A;Map position: 4
A;Introns: 35/1, 66/2, 115/3; 613/3; 694/3; 799/3; 879/3; 974/3; 1048/3; 1102/3; 1147/3;
C;Superfamily: xanthine dehydrogenase; ferredoxin [2Fe-25] homology
C;Keywords: 2Fe-25; metalloprotein
F;43,48,51,86/Binding site: 2Fe-25 cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE004642; GB:AE004091; NID:g9948163; PIDN:AAG05539.1; GSPDB:GN001]
A;Experimental source: strain PAO1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 07-Dec-1999
                                                                                                                                                  A;Reference number: 216992
A;Accession: T10236
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1364 <BEV>
A;Cross-references: EMBL:AL079347; GSPDB:GN00062; ATSP:T11111.140
A;Experimental source: cultivar Columbia; BAC clone F11111
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: T49717
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-79 < SCK1>
A, Cross-references: BMBL: AL356172, GSPDB:GN00116; NCSP: B23L21.300
A, Experimental source: BAC clone B23L21; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 2; Length 1364;
Pred. No. 61;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 35;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPDINP-WFLQR 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 DLNPLWMASR 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DINPAWYASR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-664 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
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A.Map position: 4
A.Map position: 43/1, 110/3; 608/3; 689/3; 794/3; 874/3; 969/3; 1043/3; 1097/3; 1142/3; 2.
C.Superfamily: xanthine dehydrogenase; ferredoxin [2Fe-2S] homology
C.Keywords: 2Fe-2S; metalloprotein
F;37-82/Domain: ferredoxin [2Fe-2S] homology <FDX>
F;37-82/Domain: ferredoxin [2Fe-2S] homology <FDX>
F;51,56,59,81/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xanthine dehydrogenase homolog T1111.130 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Spacession: T10235 Requence_revision 16-Jul-1999 #text_change 21-Jan-2000 (C.Spacession: T10235 Reference T1023
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                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C24G6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dacesion: T33175
R;Greco, T.; Bradshaw, H.; Keppler, D.
Submitted to the BMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C24G6.
A;Reference number: Z21298
A;Accession: T33175
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: L527 <GRE>
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            Gaps
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A;Residues: 1-1359 <BEV>
A;Cross-references: EMBL:AL079347; GSPDB:GN0062; ATSP:T11111.130
A;Experimental source: cultivar Columbia; BAC clone F11111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xanthine dehydrogenase homolog T11111.140 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 2; Length 1359;
Pred. No. 61;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2; Length 527;
Pred. No. 15;
2; Mismatches 3; Indels
        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain Bristol N2; clone C24G6
        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Genetics:
A,Gene: CESP:C24G6.6
A,Map position: 5
A,Introns: 20/3; 77/1; 129/2; 208/3; 470/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNVLSAWYAGRG 381
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 70.0
Matches 7; Conservative
        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PDINPAWYASRG 13
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                                                                                                                                                               747 PDVKPAWY 754
                                                                                   2 PDINPAWY 9
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A,Gene: ATSP:T11111.130
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        Matches
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T10236
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Gaps

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yaiw protein - Escherichia coli (strain K-12)
Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cispecies: Escherichia coli
Ciscession: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
Ciscession: E4766
Riblather, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Reference 277, 1453-1462, 1997
A; Prile: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: B64766
A; Sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-364 <BLAT>
A;Cross-references: GB:AE000144; GB:U00096; NID:g1786568; PIDN:AAC73481.1; PID:g1786576;
A;Experimental source: strain K-12, substrain MG1655
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C,Species: Escherichia coli
C,Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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A;Residues: 1.364 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33851.1; PID:g13359885; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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Pred. No. 23;
0; Mismatches 3; Indels
                                  Score 42; DB 2; Length 311; Pred. No. 19;
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   Query Match
Best Local Similarity 66./*
Chest Local 6; Conservative
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Best Local Similarity 70.0%
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Best Local Similarity 70.0°
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                                                                                                                                                                                  2 PDINPAWYA 10
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[Species: Deinococcus radiodurans
[Species: Deinococcus radiodurans
[Species: Deinococcus radiodurans
[Species: 0.8 Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
[Species: 0.7 Sissen, U.A.; Heidelberg, U.F.; Hickey, E.K.; Peterson, U.D.; Dodson, R.J.;
[Swinte, O.; Eisen, U.A.; Heidelberg, U.F.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, U.C.; Fraser, C.M.
[Spience 286, 157.1577, 1999
[A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
[A;Reference number: A75250; MUID:20036896; PMID:10567266]
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A, Molecule type: DNA
A, Residues: 1-221 <WHI>
A, Cross-references: GB: AE002010; GB: AE000513; NID: g6459448; PIDN: AAF11240.1; PID: g645945
A, Experimental: source: strain R1
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C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane
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A;Molecule type: DNA
A;Rosidues: 1-311
A;Coss.references: EMBL:M83760; NID:g342485; PIDN:AAA31907.1; PID:g342488
B;Hoffmann, R.J.; Boore, J.L.; Brown, W.M.
A;Telle: A novel mitochondrial genome organization for the blue mussel, Mytilus edulis.
A;Telle: A novel mitochondrial genome organization for the blue mussel, Mytilus edulis.
A;Reference number: S28743; MUID:92354892; PMID:1386586
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C'Bate: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C'Accession: S6600, S28753
R'Hôffmann, R.J.; Boore, J.L.; Brown, W.M.
submitted to the EMBL Data Library, June 1992
A'Reference number: S66600
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Pred. No. 13;
1; Mismatches 0; Indels
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C;Superfamily: Bacillus subtilis transcription regulator paiB
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A;Molecule type: DNA
A;Residues: 1-163,'N',165-311 <BRO>
A;Cross-references: EMBL:M83760
C;Genetics:
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Best Local Similarity 56.29
Matches 9; Conservative
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Best Local Similarity
7; Conserv
C,Genetics:
A,Gene: NCSP:B23L21.300
A,Map position: 6
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A;Accession: AH0548 A;Reference number: AB0502; MuID:21534947; PMID:11677608 .
A;Accession: CiPSPECIAL CIPSPEC
C;Accession: H85532
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Crotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H8553
A;Accession: H8553
A;Accession: H8553
A;Accession: H8554
A;Seatus: preliminary
A;Residues: 1-364 <8T0>
A;Cross-references: GB:AE005174; NID:g12513218; PIDN:AAG54724.1; GSPDB:GN00145; UMGP:204
A;Cross-references: GB:AE005174; NID:g12513218; PIDN:AAG54724.1; GSPDB:GN00145; UMGP:204
A;Cross-references: GB:AE005174; NID:g12513218; A;Genetics: A
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CORRECTED DESCRIPTION PA2695 [imported] - Pseudomonas aeruginosa (strain PAO1)
C'Species: Pseudomonas aeruginosa
C'Species: Pseudomonas aeruginosa
C'Species: 15-Sep-2000
Bracession: G83309
R'Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
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A,Accession: G8331309
A,Status: preliminary
A,Molecule type: DNA
A,Residuas: 1.37 <STO>
A,FRSiduas: 1.37 <STO
A,FRSidu
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Pred. No. 23;
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Best Accountage 70.0.
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Matches
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probable amino acid transport protein yaaJ, sodium-dependent - Escherichia coli (strain FC; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Accession: 644720
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
S; Cience 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-476 <BLAT>
A,Cross-references: GB:AE000111, GB:U00036, NID:g1786181; PIDN:AAC73118.1, PID:g1786188;
A,Experimental source: strain K-12, substrain MG1655
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                                                                                                                                                                                                                                        Gaps
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C; Superfamily: sodium-dependent D-alanine/glycine transport protein
C; Superfamily: sodium-dependent D-alanine/glycine transport protein
C; Keywords: amino acid transport; transmembrane #status predicted <TM1>
F; 10-26/Domain: transmembrane #status predicted <TM2>
F; 11-207/Domain: transmembrane #status predicted <TM3>
F; 142-158/Domain: transmembrane #status predicted <TM3>
F; 18-194/Domain: transmembran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.3%; Score 42; DB 2; Length 476; 47.1%; Pred. No. 30;
                                                                                                                    Score 42; DB 2; Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;208-224/Domain: transmembrane #status predicted <TM5>F;303-319/Domain: transmembrane #status predicted <TM6>F;349-365/Domain: transmembrane #status predicted <TM7>F;341-407/Domain: transmembrane #status predicted <TM7>F;31-407/Domain: transmembrane #status predicted <TM8>F;414-430/Domain: transmembrane #status predicted <TM8>
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                                                                                                             55.3%;
70.0%;
                                                                                                                                                                              Best Local Similarity 70.0 Matches 7; Conservative
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Best Local Similarity
A; Gene: PA2695
                                                                                                                          Query Match
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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August 12, 2004, 14:37:35; Search time 3.40116 Seconds (without alignments) 199.024 Million cell updates/sec US-09-700-643A-2_COPY_12_24 76 1 TPDINPAWYASRG 13 OM protein - protein search, using sw model Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 Total number of hits satisfying chosen parameters: 141681 seqs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	14.14.00		homo	bos tau	P81278 rattus norv	P77562 escherichia	P30143 escherichia	094269 schizosacch		P34347 caenorhabdi	Q9nvr5 homo sapien	P35360 limulus pol		Q88da5 pseudomonas			helic	homod	homod	campo					СĽ	bos tauru	z ger		esche	ω	æ	Φ	Ω,	pseudomo	Q9jm10 marmota mon
SUMMAKLES	í	T. T	PRRP_HUMAN	PRRP_BOVIN	PRRP_RAT	YAIW_ECOLI	YAAJ_ECOLI	UBP3_SCHPO	CYGR_ARBPU	YK69 CAEEL	CNA4 HUMAN	OPS1_LIMPO	OPS2_LIMPO	THIC PSEPK	IMMT MOUSE	AAM1_RHOSH	PLSC HELPY	I18B_HUMAN	WNT2 HUMAN	OPSD_CAMAB	OPSD_CATBO	YEIB ECOLI	EX7L_STRCO	Y955 MYCTU	RFA1 CRIFA	ANXB_BOVIN	POLG ZYMVR	LMBT_HUMAN	YLCE ECOLI	RL31 SYNEL	PCP STAAU	AMPE ECOLI	YEAB BACSU	TRPI PSEAE	
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	% Query	Match	100.0			55.3					52.6	52.6	52.6	52.6	52.6	51.3	50.7	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	49.3	48.7	48.7	48.7			8	α
		Score	16	72	68	42	42	42	41	4	04	40	40	0.4	40	39	38.5	(7)	38	38	38	38	38	38	38	38	38	37.5	• • •	3.7	37	3.7	3.7	37	
	Result	S S	H	7	m	4	ហ	9	7	- αο	ט	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26	27	23	29	30	31	32	33

Q9h209 homo sapien P73879 synechocyst O82947 chromatium C09309 caenorhabdi P56592 canis famil P31795 radiation m P21517 escherichia Q9ukuO homo sapien Q43007 akr murine C54468 serratia ma Q10068 schizosacch
O
OAA4 HUMAN Y264_SYNY3 CYCR_CHRVI CYCZ_CARVI CP12_CANFA POL_MURK MALZ_ECOLI LCFF_HUMAN PDA1_ORYSA POM MIVAK CHB_SERMA
OAAA Y264 CYCR, YOSI, CP12, CP12, POL, ICCP PDAI, POL
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## ALIGNMENTS

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us-09-700-643a-2_copy_12_24.rsp

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Rattus norvegicus
                                                                                                  NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.
                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              Fukusumi S.,
                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION (G-54 PROVIDE AMIDE GROUP) 08AC35A13B0FA908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
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Hormone; Amidation; Signal; Cleavage on pair of basic residues.
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                                                                                                                                                                                                                                                                                                                                                                                                       Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fuk
Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
Kurokawa T., Nishimura O., Onda H., Fujino M.;
"A prolactin-releasing peptide in the brain.";
                 100.0%; Score 76; DB 1; Length 87; 100.0%; Pred. No. 3.9e-06;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.1e-05;
0; Mismatches 1; Indels
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                                                                                                                                                                 98 AA
                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98268781; PubMed=9607765;
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PRRP RAT

D PRRP RAT

AC P81278; Q8K3YO;
DT 30-MAY-2000 (Rel. 39, Last sequent)

DT 30-MAY-2000 (Rel. 39, Last annota)
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Query Match
Best Local Similarity 100.0.
e..hes 13; Conservative
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                                                                    1 TPDINPAWYASRG 13
                                                                                              TPDINPAWYASRG 46
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                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                            releasing peptide PrRP20
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NCBI_TaxID=9913;
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33
58
53
98 AA;
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                                                                                                                                                    BOVIN
                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                             PRRP_BOV
P81264;
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PEPTIDE
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Matches
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Last sequence update) Last annotation update)

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STRAIN-Sprague-Dawley; TISSUE-Hypothalamus;
Anderson S.T., Kokay I.C., Lang T., Grattan D.R., Curlewis J.D.;
"Quantitation of prolactin-releasing peptide (PrRP) mRNA expression in specific brain regions during the rat cestrous cycle and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION (G-53 PROVIDE/AMIDE GROUP).
TPDINPAWYTGRGIRPVGRFGRRRATPRDVTGLGQLSCLPL
DGRTKFSQRG -> SECLTYGKQPLTSFHPFTSQMPP (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEGUL PEPT. 83:1-10(1999).

-!- FUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactotrophs directly to secrete PRL.

-!- ALTERNATIVE PRODUCTS:

-:- ALTERNATIVE PRODUCTS:

-- ALTERNATIVE PR
                                                                                                                                                                                                                                                                                                                                                  Rattus nozvegytus (mar.).
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.; M., Prolactin releasing peptide in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY.
MEDLINE=99426652; PubMed=10498338;
Pujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sumino Y., Fujino M.;
"Tissue distribution of prolactin-releasing peptide (PrRP) and its
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Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing peptide PrRP20].
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-!- TISSUE SPECIFICITY: Widely expressed, with highest levels in medulla oblongata and hypothalamus.
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PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
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                                                                                                                                                                 Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68; DB 1; Length 83;
Pred. No. 8.3e-05;
0; Mismatches 2; Indels
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        DOC75A264EEE4F29 CRC64;
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MEDLINE=98268781; PubMed=9607765;
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Best Local Similarity 84.6%;
Matches 11; Conservative
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        SEQUENCE
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SEQUENCE FROM N.A.
STRAIN=K12 / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A., Systematic sequencing of the Escherichia coli genome: analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Potential).
-!- SIMILARITY: BELONGS TO THE SODIUM:ALANINE SYMPORTER FAMILY (SAF). STRONG, TO H.INFLUENZAE HI0183.
                                                                                                                                                                                 the 0-2.4 min region.";
Nucleic Acids Res. 20:3305-3308(1992)
                                                                                      MEDLINE=92334977; PubMed=1630901;
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Best Local Similarity
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UBP3_SCHPO
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Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,

Duncan M., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D.,

Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Viannes J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Pred. No. 9.4;
0; Mismatches 3; Indels
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Mau B., Shao Y.;
MThe complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, U73857; AAB18101.1; -.
PIR, B64766; B64766.
EcoGene; EG13608; yaiw.
Interpro; IRR00437; Prok_lipoprot_S.
Hypothetical protein; Complete professe.
SEQUENCE 364 AA; 40414 MW; 7170FAF05C4E5973 CRC64;
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YAA_ECOLI

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AC PROJA;

DT 01-UL-1993 (Rel. 26, Created)

DT 01-UL-1993 (Rel. 26, Last sequence update)

DT 28-FEBS-2003 (Rel. 41, Last annotation update)

DE Putative transporter yaaJ.

GN YAAJ OR B0007.
                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                       Hypothetical protein yaiw.
YAIW OR B0378.
Escherichia coli.
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                       33 TPDINPAWYTGRG 45
                                                                                                                                                                                           STANDARD;
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                             TPDINPAWYASRG
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STRAIN=K12 / MG1655;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its modified by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     TICRFAMS; TICRO0835; agcS; 1.
PROSITE; PSO0873; NA ALANINE_SYMP; 1.
Hypothetical protein; Transmembrane; Inner membrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
9
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Last annotation update)
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; Mismatches
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EMBL; AE00111; AAC73118.1; --
ENGGERE; EG4720; G4720.
ECGGERE; EG11555; yaaJ.
Interpro; IPR002293; AA/rel_permeasel.
Interpro; IPR001463; Na/Ala_Symport.
Pfam; PF01235; Na Ala_Symp; 1.
PRINTS; PR00175; NAALĀSMPORT.
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(Rel. 41, Last seq.
(Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 DVNGQFRGGPAWYMARG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 DIN-----PAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Symport; Complete proteome.
TRANSMEM 4 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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361 PEILPEWHSSKG 372

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RA WOOd V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Goulcos J., Peat N., Hayles J., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornes M., Leather S., McLean J.,
James K., Jones L., Jones M., Leather S., McDomaid S., McLean J.,
RA Mooney P., Mouil S., Pearson D., Quail M., Rabhiowatsch E.,
RA Rutherford K., Rutter S., Saudres S., Stevens K.,
RA Raylor K., O'Neil S., Pearson D., Quail M., Rabhiowatsch E.,
RA Skelton J., Yolckeart G., Art R., Robben J., Grymonprez B.,
Waodward J., Volckeart G., Art R., Robben J., Grymonprez B.,
RA Woodward J., Volckeart G., Art R., Robben J., Grymonprez B.,
RA Weltjens I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goble C., Roben S., J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Codieu A., Cadieu E., Dreane S., Gloux S., Lelaure V., Mottier S.,
RA Lotas M., Rocher T., McCombie W. R., Paulsen I., Potashkin J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Crutti L., Lowe T., McCombie W. R., Paulsen I., Potashkin J.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F.,
RA Daga R.R., Cruzado L., Jimenez S., Armetrong J., Rorsburg S.L.,
RA Daga R.R., Cruzado L., Jimenez S., Armetrong J., Rorsburg S.L.,
RA Daga R.R., Cruzado L., Jimenez S., Armetrong J., Rorsburg S.L.,
RA Daga R.R., Cruzado L., Jimenez S., Armetrong J., Rorsburg S.L.,
RA Daga R.R., Cruzado L., Jimenez S., Armetrong S., Arm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Probable ubiquitin carboxyl-terminal hydrolase 3 (EC 3.1.2.15) (Ubiquitin thiolesterase 3) (Ubiquitin-specific processing protease 3) (Deubiquitinating enzyme 3). UBP3 OR SPBP8B7.21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSTITE PROGRASS UCH 2 1: 1.
Ubl conjugation pathway; Hydrolase, Thiol protease, Multigene family.
ACT SITE 142 142 BY SIMILARITY.
ACT SITE 445 453 BY SIMILARITY.
SEQUENCE 512 AA; 58081 MW; 1F97DA2C7720695D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 1; Length 512;
Pred, No. 13;
4; Mismatches 2; Indels
                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenebB_SPonbe; SPBP8B7.21; -. GO; GO:0006464; P:protein modification; ISS. GO; GO:0006508; P:proteolysis and peptidolysis; ISS. InterPro; IPR001394; Peptidase_C19.
                                                                                                                                                                                                                                                                                                                     MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL032684; CAA21806.1; -. PIR; T40815; T40815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.3%;
                                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                 NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                             Resact receptor precursor (Guanylate cyclase) (EC 4.6.1.2).
Arbacia punctulata (Punctuate sea urchin.)
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Arbacoida; Arbaciidae; Arbacia.
                                                                                                                                                                                                        Singh S., Lowe D.G., Thorpe D.S., Rodriguez H., Kuang W.-J., Dangott L.J., Chinkers M., Goeddel D.V., Garbers D.L., "Membrane guanylate cyclase is a cell-surface receptor with homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                           CYTOCHASTAL

PROTEIN KINASE LIKE,
N-LINKED (GLCNAC, .) (POTENTIAL)
N-LINKED (GLCNAC, .) (POTENTIAL)

TOTAL (GLCNAC, .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000001; Prot kinase; 1.
PROSITE; PSS0011; PROTEIN KINASE_DOM; 1.
Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41, DB 1, Length 986;
Pred. No. 38;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESACT RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111284 MW; B40238A74CCAFC52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                           986 AA.
                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                           MEDLINE=88318927; PubMed=2901039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR, SO5480, OYURGA.
InterPro; IPR001828; ANF receptor.
InterPro; IPR001054; G_Gyclase.
InterPro; IPR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X12874; CAA31367.1; -.
                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cGMP biosynthesis; Si
SIGNAL 1 2
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568
185
185
361
410
986 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
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                          ARBPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
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TRANSMEM
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CARBOHYD
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CARBOHYD
SEQUENCE
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RESULT 7
CYGR ARBPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                          CYGR
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                                    В
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6; Conservative

RESULT 8 YK69_CAEEL

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Gaps

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2; Indels

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0
                                                                                                                                                                                                                                                      Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer B., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ပ်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            >
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S44765; S44765.
Wormbep; C29E4.9; CE29199.
Hypothetical protein.
SEQUENCE 208 AA; 23729 WW; FD4A57F6609EEB32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 1;
Pred. No. 12;
1; Mismatches 4
                             01-FEB-1994 (Rel. 28, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C2964.9 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNA4 HUMAN STANDARD; PRT; 328 AA. 099NVR5; Q8GTY8; Q969Z5; 10-0CT-2003 (Rel. 42, Loreated) 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update)
208 AA
                                                                                                                                                                                                                            STEAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L23651; AAA27956.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 TEVVNPAAYAQRG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein C14orf104.
C14ORF104.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
 YK69 CAEEL
P34347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
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EXECUTEDENCE FROM: W.A. (LOUTOKOW 2/)

RE TISSUE=BORNE MAINEY, W.A. (LOUTOKOW 2/)

RE STRAUSER R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Attauner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buendlo M.F., Casvant T.L., Scheefer T.E.,

RA Batchenco M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheefer T.E.,

RA BAN S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA BAS S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubs R.A.,

RA Richards S., Worley K.C., Hae S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hae S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Halton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibs R.A.,

RA Fahey J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

RA Halton M.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length human

RA Manney And Manney R. W., Rodrigues M. R.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                 Heilig R., Eckenberg R., Petit J.-L., Fonknechten N., Da Silva C., RA Heilig R., Eckenberg R., Patit J.-L., Fonknechten N., Da Silva C., RA Heilig R., Eckenberg R., Barbe V., De Berardinis V., Ureta-Vidal A., RP Pelletier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S., RA Sun H., Du H., Pepin K., Attiguenave F., Robert C., Cruaud C., Cruaud C., Bruels T., Jaillon O., Friedlander L., Samson G., Brottier P., RA Aiach N., Boscus D., Dickhoff R., Dors M., Dubois I., Friedman C., RA Aiach N., Bellemer F., Samins N., Dubois I., Friedman C., RA Aiach N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Trask B., RA Martins N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Trask B., Aucherie B., Bellemere C., Belser C., Besnard-Gonnet M., Acherie B., Bellemer C., Lechaplais C., Louesse C., Muselet D., RA Dufosse-Laurent V., Ferron C., Lechaplais C., Louesse C., Muselet D., RA Wagdelenat G., Petra B., Petit E., Strvain-Trukniewicz P., Trybou A., RA Robert D., Wunderle E., Petit E., Brodelais I., Dubois M., Avedier J., Werdier-Discala C., Hillier L.M., Fulton L., McPherson J., A Verdier D., Walerston R., Hood L., Weissenbach J., A Quetier F., Materston R., Hood L., Weissenbach J., Runne 421:601-607(2003).

Nature 421:601-607(2003).
Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Salto K., Yamamoto J., Wakamura L., Nakamura Y., Nagamoto Y., Nagantsu A., Nakamura Y., Nagauto Y., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project.";
                                                                                                                                                                                                                                 TISSUE-Neuroblastoma;
Li W B., Gruber C., Jessee J., Polayes D.;
"Full-length oDNA libraries and normalization.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q9NVRS-2; Sequence=VSP_008390;
Note=May be due to exon skipping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lsoId=Q9NVR5-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                     (ISOFORM 2).
                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                  SEQUENCE
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Transmembrane, Glycoprotein; Vision;

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Photoreceptor; Retinal
                                    Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIMPO
                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                             DOMAIN
TRANSMEM
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TRANSMEM
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DISULFID
                                                                                                                                 FRANSMEM
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                                                                                                                                                                                FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPS2_LIMPO
ID OPS2_LIMI
AC P35361;
                                                                                                            DOMAIN
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
             ð
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       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE-93317641, Pubmed-8327495,

A Smith W.C., Price D.A., Greenberg R.M., Battelle B.-A.;

T. Mopsins from the lateral eyes and ocelii of the horseshoe crab,

T. Limulus polyphemus.";

T. Limulus polyphemus.";

Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993).

-!- FUNCTION: Visual pigments are the light-absorbing molecules that mediate vision. They consist of an apoprotein, opsin, covalently linked to cis-refinal.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- FISSUE SPECIFICITY: LATERAL EYE.

-!- PTM: Some or all of the carboxyl-terminal Ser or Thr residues may be phosphorylated (By similarity).

-!- MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM AT 520 NM.

-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Lateral eye opsin.
Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazos; Arthropoda; Chelicerata; Merostomata; Xiphosura; NCBL TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                 52.6%; Score 40; DB 1; Length 328; 60.0%; Pred. No. 18; 3; Indels ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                     Missing (in isoform 2).
/FTId=VSP_008390.
87875CEZA89AF663 CRC64;
ities requires a license agreement (Ssend an email to license@isb-sib.ch).
                                                                    EMBL, AK001425, BAA91684.1; -.
EMBL, BX248264; CAD62592.1; ALT INIT.
EMBL, AL139099; -; NOT ANNOTATED_CDS.
EMBL, BC013322, AAH13322.1; -.
EMBL, BC011400; AAH11400.1; -.
Genew, HGNC:20188; C140rf104.
                                                                                                                                                                                                                                                                                                    328 AA; 36943 MW;
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 60.0
les 6; Conservative
                                                                                                                                                                                                                                                     160
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 DINPAWYASR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                          Alternative splicing
VARSPLIC 113 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLNPLWYKLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
  SPET TENENCY SOLUTION OF THE SECOND S
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PEGM. PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50226; G PROTEIN RECEP F1 2; 1.
PROSITE; PS00238; OFSIN; 1.

EMBL, L03791, AAA28273.1; -.
EMBL, L03781, AAA02498.1; -.
EMBL, EDST, BABLIF.
HSSP, P02699, 1EDV.
InterPro, IPR000276; GPCR Rhodpsn.
InterPro, IPR001760; Opsin.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Limitus polyphemus.",

Proc. Natl. Acad. Sci. U.S.A. 90:6150-6154(1993).

- PUNCTION: Visual pigments are the light-absorbing molecules that mediate vision. They consist of an apoprotein, opsin, covalently linked to cis-retinal.

- SUBCELLIUAR LOCATION: Integral membrane protein.

- SUBCELLIUAR LOCATION: Integral membrane protein.

- PTM: Some or all of the carboxyl-terminal Ser or Thr residues may be phosphorylated (By similarity).

- MISCELLANEOUS: THIS OPSIN HAS AN ABSORPTION MAXIMUM AT 530 NM.

- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ocellar opsin.
Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                              RETINAL CHROMOPHORE (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUB-Median ocelli,
MEDLINE-93317641; PubMed-8327495;
Smith W.C., Price D.A., Greenberg R.M., Battelle B.-A.,
"Opsins from the lateral eyes and ocelli of the horseshoe crab,
                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                     52.6%; Score 40; DB 1; Length 376, 50.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                  CCE401766AB06F26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
etinal protein, Transmembrar
G-protein coupled receptor
46 EXTRACELLULAR.
71 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 21;
2; Mismatches
                                                                    CYTOPLASMIC.
2 (POTENTIAL)
                                                                                                       EXTRACELLULAR
3 (POTENTIAL)
                                                                                                                                                         4 (POTENTIAL)
EXTRACELLULAR
                                                                                                                                                                                                                                                EXTRACELLULAR
                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                              7 (POTENTIAL)
                                                                                                                                                                                                                                                                                 CYTOPLASMI
                                                                                                                                            CYTOPLASMI
                                                                                                                                                                                                           CYTOPLASMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                    42139 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L03792; AAA28274.1; -. EMBL; L03782; AAA02499.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPMNPLWYSILG 51
                                      46
71
83
83
108
123
162
186
                                                                                                                                                                                                                                                                                                                                   17
193
376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                           332
332
120
318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6850;
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-!- SIMILARITY: Belongs to the thiC family.
                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida XT2440.";
Environ. Microbiol. 4:79-808(2000).
Environ. Microbiol. 4:79-808(2000).
-i. FUNCTION: Required for the synthesis of the hydromethylpyrimidine (HPP) moiety of thiamine (4-amino-2-methyl-5-hydroxymethylpyrimidine) (8y similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nartins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson M., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Haim S.,
Fraser C.M.;
                                                                                             Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision; Phosphorylation; G-protein coupled receptor.

1 46 EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                           RETINAL CHROMOPHORE (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                 52.6%; Score 40; DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                             FA9647C40531CBF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
17-MAR-2004 (Rel. 43, Last annotation update)
THIC OR PP4922
                                                                                                                                                                       3 (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                                                                                    S (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                                                                                                                              7 (POTENTIAL).
                                                                                                                               1 (POTENTIAL).
                                                                                                                                                  2 (POTENTIAL).
EXTRACELLULAR.
                                                                                                                                                                                                        EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                             InterPro; IPR001760; Opsin.
PEam, PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHDODPSN.
PROSITE; PS00237; G PROTEIN_RECEP_F1 1; 1.
PROSITE; PS50252; G PROTEIN_RECEP_F1 2; 1.
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                           4 (POTENTIAL)
                                                                                                                                                                                                                                                 EXTRACELLULAR
                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                        CYTOPLASMIC
         HSSP; P02699; 1EDV.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Opsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas putida (strain KT2440)
                                                                                                                                                                                                                                                                                                                               42111 MW;
                                                                                                                                                                                                                                                                                                                                                            50.0%;
                                                                                                                                                                                                                                                                                                                                                           Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                            2 PDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                  40 PPMNPLWYSILG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
 PIR; A48197; A48197.
                                                                                                                                                                                                                                                                                                      17
193
376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCB1_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THIC PSEPK
                                                                                                                                          DOMAIN
TRANSMEM
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                        DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                              RANSMEM
                                                                                                                                                                                                                                                                                   DISULPID
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388D<u>A</u>5;
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          THIC PSEPK
                                                                                                                                                                                                                                                                                                                                                                        Matches
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RADIURE_STAGESTS PubMed=12466851;

RADIURE_STAGESTS PubMed=12466851;

RADIURE_STAGESTS PubMed=12466851;

RADIURE_STAGESTS PubMed=12466851;

RADIURE_STAGESTS PubMed=12466851;

RADIURE_STAGESTS PubMed=12466851;

RADIA STAGESTS PubMed=1246851;

RADIA 
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"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%; Score 40; DB 1; Length 626; 50.0%; Pred. No. 36; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAR, MF 00089; -; 1.
InterPro_IPR002817; ThiC.
Pfam, PF01964; ThiC; Thiamine biosynthesis; Complete proteome.
SEQUENCE 626 AA; 69727 MW; E22CBAAEGB8D6313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBCAGB; QBC7V1; QBCCIO; 10-OCT-2003 (Rel. 42, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last ennotation update) Mitochondrial inner membrane protein (Mitofilin).
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE016792; AAN70489.1; -.
TIGR; PP4922; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 50.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 PDVRSAWIEARG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I MMT MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20428429; PubMed=10970853;
Shah D.S.H., Porter S.L., Martin A.C., Hamblin P.A., Armitage J.P.;
Shah D.S.H., Porter S.L., Martin A.C., Hamblin P.A., Armitage J.P.;
"Fine tuning bacterial chemotaxis: analysis of Rhodobacter sphaeroides
behaviour under aerobic and anaerobic conditions by mutation of the
major chemotaxis operons and cheY genes.";
EMBO J. 19.4601-4613(2000)
-:- SIMILARITY: Belongs to family 13 of glycosyl hydrolases. GlgB
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEAFSSSVRERPPEEVAARLAQQEKQEQVEMES -> A
                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q8CAQ8-3; Sequence=VSP_007003, VSP_007004, VSP_007005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform 2 and isoform 3). /FIId=VSP_007003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobactera. (CBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
 SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 1; Length 757; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FIId=VSP_007004.
SISDLA -> T (in isoform 3).
/FIId=VSP_007005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5EB37BCA054BD7A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides)
                                                                                                                                                                          Note=No experimental confirmation available;
                                                                                                            IsoId=Q8CAQ8-2; Sequence=VSP_007003;
Note=No experimental confirmation available;
               similarity).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative glycosidase (EC 3.2.1.-) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            678 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (in isoform 3 / FTId=VSP 007
                                                                               IsoId=Q8CAQ8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                    EMBL, AK033126; BAC28163.1; -. BMBL; AK038129; BAC29356.1; -. EMBL; AK049189; BAC33599.1; -. MGD; MGI:1923864; Immt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequ
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                757 AA; 83900 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 75.0
nes 6; Conservative
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757
151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387
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Q9JN46;
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                                                              Name=1;
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAINES FROM N.A.

STRAINES 6695 / ATCC 700392;

STRAINES 6794467; PubMed=9252185;

MEDLINE=97934467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Goodyne J.D., Utterback T.R., Peterson J.D., Kelley J.W.,

Cotton M.D., Weidman J.M., Fulii C., Bowman C., Watthey L., Wallin E.,

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-2003 (Rel. 41, Last sequence update)
1-acyl-sn-qlycerol-3-plosphate acyltransferase (EC 2.3.1.51) (1-AGP acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The complete genome sequence of the gastric pathogen Helicobacter
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                                                                                                                                                                                                                                                             51.3%; Score 39; DB 1; Length 678; 53.8%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                             678 AA; 77092 MW; E88EBD0339F1B61D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 AA.
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                                                                                                                                              InterPro; IPR006047; Alpha amyl cat. Ffam; PF00128; alpha amylase; 1. Hydrolase; Glycosidase.
                                                                                                                                  EMBL; X80205; CAB87126.1; -.
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                                                                                                                                                                                                                                                                                                                                                                            546 TPDINPVYLQHSG 558
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.00
To Conservative
                                                                                                                                                                                                                                                                                                                                          1 TPDINPAWYASRG 13
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EMBL; AE000636; AAD08393.1; -. PIR; D64688; D64688.

This SWISS-PROT entry is copyright. It is produced through a collaboration

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DR TIGR; HP1348; -.

DR InterPro; IPR002123; Acyltransferase.

DR InterPro; IPR0045213 Acyltransferase.

DR InterPro; IPR00452; AGP acyltrn.

DR Pfam; PP01553; Acyltransferase; 1.

DR SMART; SM0563; P18C; 1.

DR TIGRAMS; TIGR00530; AGP acyltrn; 1.

XW Phospholipid biosynthesis; Transferase; Acyltransferase;

XW Inner membrane; Complete proteome.

SQ SEQUENCE 240 AA; 27745 MW; 22BD5D0EB190BBDD CRC64;

Query Match

S0.7%; Score 38.5; DB 1; Length 240;

Best Local Similarity 70.0%; Pred. No. 24;

Matches 7; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

DD 208 TPDIN-PAMY 9

DD 208 TPDINSPTWY 217
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Search completed: August 12, 2004, 14:44:52 Job time : 3.40116 secs

OM protein

Run on:

Sequence:

Searched:

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Q8guq8 arabidopsis
Q9gw45 arabidopsis
Q99m45 pseudomonas
Q9t559 meurospora
Q9t659 mytilus cal
Q9t531 mytilus cal
Q9t53 deinococcus
Q9t53 deinococcus
Q9t639 pseudomonas
Q82y3 pseudomonas
Q82y3 pseudomonas
Q82y3 xanthomonas
Q82y3 xanthomonas
Q82y6 arathomonas
Q8764 secherichia
Q8.56 escherichia
Q8.575 salmonalla
Q8.717 xenopus lae
Q8.718 mus musculu
Q8.875 escherichia
Q8.717 xenopus lae
Q8.718 mus musculu
Q8.875 escherichia
Q8.875 escherichia
              Q8gz21 arabidopsis
Q8a693 bacteroides
Q8x0r0 neurospora
Q9sw46 arabidopsis
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Ovis aries (Sheep).
Usukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Curlewis J.L., Anderson S.T.; Curlewis J.D., Kusters D.H.L., Barclay J.L., Anderson S.T.; "Prolactin-releasing peptide (PrRP) in the ewe: cDNA cloning, midistribution and effects on prolactin secretion in vitro and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 98;
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Pred. No. 0.00017;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF450453; AAL47178.1; -. SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAAB5 CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                 QBSR31
Q9RTS3
Q9BJL8
Q88GB9
Q882X3
Q882X3
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Q8FKE5
Q8Z8Z7
                                                                                                                                                                                                                                                                                                                                                     Q83MA5
Q910E7
Q7ZTL7
Q9KIW3
Q8GZ21
Q8A693
Q8X0R0
                                                                 Q9SW46
Q8GUQ8
Q9SW45
Q9I1W4
Q9P5J9
                                                                                                                                                                                                                                                                   Q8P501
Q8ZRF4
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088854
088802
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Local Similarity 92.3%;
les 12; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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     Bovidae, Caprina
NCBI_TaxID=9940;
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01-NOV-1999
01-DEC-2001
     Query Match
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Q9W624;
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Q8WN12;
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                                                                                                                        August 12, 2004, 14:37:35 ; Search time 17.9128 Seconds (without alignments) 228.984 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                            1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                          US-09-700-643A-2_COPY_12_24
76
1 TPDINPAWYASRG 13
                                                                                            - protein search, using sw model
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QQW624
QQW624
QGOWW85
QQUWN85
QQWW85
QTWUL5
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QT
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sp_wortebrate:*
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Gapop 10.0 , Gapext 0.5
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sp_fungi:*
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Maximum DB seq length: 200000000
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sp_mhc:*
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Match
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                                                                                                                                                                                                                 Perfect score:
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Database :

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Gaps

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Result No.

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The Property of the Property of the Sushi-repeat containing protein and characterization of the sushi-repeat containing protein and characterization of the sushi-repeat containing protein an Cloning and characterization of the sushi-repeat containing protein and Cloning and characterization of the sushi-repeat containing protein and CRCO, ";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

Brabl, AF303649; AAC13765.1; -

BRBL, AF333649; AAC13655.1; -

CO:0006118; P:electron transport; IEA.

RRIL, AF33349; AAM13693.1; -

CO:0006118; P:electron transport; IEA.

RILEPPO: IPR001128; Cytcchrome_P450.

RILEPPO: IPR001128; Sushi SCR_CCP.

R InterPro: IPR00044; Sushi SCR_CCP.

R Pfam; PF00084; sushi; 3.

R PFam; PF00084; sushi; 3.

R PROSITE; PS00086; CYTOCHROME P450; 1.
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Best Local Similarity
7; Conserve
      SEQUENCE FROM N.A.
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TISSUE=Placenta;
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les 7; Conserv
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ID Q20170
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                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A.
KUNCSAWA H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjyo T., Rakestraw K.M., Naeve C.W., Look T.A.; Submitted (APR-1998) to the BWBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.5%; Score 49; DB 13; Length 117; 53.8%; Pred. No. 1.5; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 54;
                                                                                                                                                                                                                                           TISSUE-Brain;
Satake H., Minakata H., Fujimoto M.;
Carassius RFamide (C-FF amide).";
Carassius RFamide (C-FF amide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; --
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawlor S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035608; CAB55682.1; -.
NON TER 54 54
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01-AUG-1998 (TrEMBLrel, 07, Last sequence update)
01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
Sushi-repeat protein (Sushi-repeat containing protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 54 AA; 6110 MW; B2F3C39F7B961A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-001-2003 (TrEMBLrel. 25, Created)
01-001-2003 (TrEMBLrel. 25, Last sequence update)
01-001-2003 (TrEMBLrel. 25, Last annotation update)
DJ479J7.3 (Sushi-repeat protein (SRPUL)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 4;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                Carassius auratus (Goldfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.8%;
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56 SPEIDPFWYVGRG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TPDINPAWYASRG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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060687
1D 06068
AC 06066
AC 06066
DT 01-AP
DT 01-AP
DT 01-AP
DE SUSH;
CO EUKR:
OC EUKR:
OC Mamm
OX NCB!
RP [1]
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Strausberg R.,
Strausberg R.,
Strausberg R.,
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BEO20733; AAH20712.
GO, GO:0066118, P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR003410; Hyalin.
Pfam; PF02494; HYR; 1.
R Pfam; PF02494; HYR; 1.
R Pfam; PF02494; HYR; 1.
R Pfam; PF000044; sushi, 3.
R SMART; SM00032; CCP, 3.
RPOSITE; PS00066; CYTOCHROME_P450; 1.
SEQUENCE 465 AA; 52957 MW; 3D7229487DAlB8BD CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. Corresponding sequence F38E11.7).
WRT-3.
      Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 465;
                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Sushi.-repeat protein.
Homo sapiens (Human)
Score 47; DB 4;
Pred. No. 14;
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53.8%; Pred. No. 14;
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10

Query Match

OCC OCC OX REPRESENT REPRE

Best Loc Matches

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Q7XMH8;

Q7XMH8

RESULT 7 27 XMH8

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Parkill J., Sebaihia M. Preston A., Murphy L.D., Thomson N.,
A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
A Gerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
A Achtan M., Arkin R., Baker S., Basham D., Bason N., Cherevach I.,
A Hillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Peltwell T., Goble A., Hamlin N., Hauser H., Holloyd S., Jagels K.,
I leather S., Moule S., Norberzak H., O'Neil S., Ormond D., Price C.,
A Rabbinowitsch E., Ruter S., Sanders M., Saunders D., Seeger K.,
A Dimmond M., Skelton J., Squares S., Stevens K.,
A Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
Tomparative analysis of the genome sequences of Bordetella pertussis,
I Nat. Genet. 35:32-40(2003)

Transferase, Complete proteome.

Transferase, Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                          Bordetella pertussis.
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Alcaligena, Proteobacteria.
NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%; Score 44; DB 16; Length 432; 64.3%; Pred. No. 42; 7xive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 16; Length 387; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Complete protecme.
SEQUENCE 432 AA; 46834 MW; D86B8323A85FCA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 AA; 42002 MW; 91F207251B1A4C94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) S-adenosylmethionine synthetase (EC 2.5.1.6).
                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=TOHAMA I / ATCC BAA-589 / NCTC 13251;
MEDLINE=22827954; Pubmed=12910271, Mischin
S-adenosylmethionine synthetase (EC 2.5.1.6)
METK OR BP3071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 37;
1; Mismatches
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(TrEMBLrel. 25, Last seq.
(TrEMBLrel. 25, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=RBSO / ATCC BAA-588;
MEDLINE=22827954; PubMed=12910271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.9%;
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Best Local Similarity 64...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=518;
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01-0CT-2003
01-0CT-2003
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Q7WQX8;
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Fr G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.O., Zhu G.F., Tu Y.F., Jia G., Wang S.Y., Rang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q., Huang Y.G., Li Y., Zhu G., Lu Y., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H., Oian Y.M., Ying X., Zhu Y., Li Y., Liu Y.Q., Yu S.L., Liu X.H., Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang Y., Hu H., Jia P.X., Chang R.Q., Guan J.P., Hong G.F., The P.N., Alace S. Shomitted (DEC-2001) to the EWBL/GenBank/DDBJ databases.
EWBL, Alace2944, Che04622 l., ED04CAF2E989700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
             Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 179;
                                                                                                                                                                                 the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                         Matthews P.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                   EMBL; Z68342; CAA92775.2; -.
SEQUENCE 179 AA; 20965 MW; F9FA6891A2BF2BDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   816 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                               59.2%; Score 45; DB 75.0%; Pred. No. 11; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                 Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                     STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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(TrEMBLrel. 25, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                               "Genome sequence of the nemi
investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSJNBa0028123.4 protein.
OSJNBA0028123.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDVKPAWY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PDINPAWY 9
                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                 SEQUENCE FROM N.A.
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                                                       NCBI_TaxID=6239;
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Q7VULS;

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Q7VULS

RESULT 8 Q7VULS

Query Match

RESULT 10 Q7W200

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"General sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).

EMBL; AE009813; AA163376.1; -
GO; GO:000474; F:malate synthase activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:000619; P:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
GO; GO:0006809; P:tricarboxylate cycle; IEA.
InterPro; IPR000465; Lipochl. CytFABP.
InterPro; IPR000465; Malate synthase.
PF01274; Malate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-INA. / ATCC 51768 / DSM 7523;
MEDIJINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.9%; Score 44; DB 5; Length 527;
58.3%; Pred. No. 52;
Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 17; Length 813;
Pred. No. 83;
Greco T., Bradshaw H., Keppler D.;
"The sequence of C. elegans cosmid C24G6.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                             Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL, AF067936; AAC19213.1; -PIR; T33175; T33175.
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SEQUENCE 813 AA; 93836 MW; 1EB05EA41EA06FE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                            WormPep; C24G6.6; CE17462.

WormPep; C24G6.6; CE17462.

GO; GO:0006118; P:ed-ectron transport; IEA.

InterPro; IPR00293; Amino oxidase.

InterPro; IPR002035; NAD BS.

Pfam; PF01593; Amino oxidase; 1.

Hypotherical protein oxidase; 1.

SEQUENCE 527 AA; S9805 MW; 9FBBIFB6443
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Pfam; PF01274; Malate synthase;
PROSITE; PS00213; LIPOCALIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea, Crenarchaeota; Thermo
Thermoproteaceae, Pyrobaculum.
NCBI_TaxID=13773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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01-MAR-2002 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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                                                                                                                                                                      Waterston R.; "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malate synthase (glcB)
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les 7; Conserv
                                                                                                                SEQUENCE FROM N.A. STRAIN-Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
A Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
A Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
A Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
Rabbinowitsch E., Norberczak H., O'Neil S., Ormond D., Price C.,
A Rabbinowitsch E., Sharrell B.G., Maskell D.J.;
Comparative analysis of the genome sequences of Bordetella pertussis,
T. "Comparative analysis of the genome sequences of Bordetella pertussis,
D. Natt. Genet. 35:32-40120033
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                       METK OR BPP0192.
Bordetella parapertussis.
Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=519;
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Pred. No. 42;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEC. BENBL, BX660423; CAB39933.1; -.
Transferase; Complete proteome.
SEOUENCE 432 AA; 46834 MW; D86B8323A8SFCA9D CRC64;
                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) S-adenosylmethionine synthetase (EC 2.5.1.6).
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                             432 AA.
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                                                                                                                                                                                                                                                                                      Created)
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=12822 / ATCC BAA-587;
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                                                                                                                                                                                                                                                                             (TrEMBLrel. 25,
                                                                        180 TPDLMPAPIWYAHR 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 TPDLMPAPIWYAHR 193
                        1 TPDINPA--WYASR 12
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Matches 9; Conservative
                                                                                                                                                                                                                          PRELIMINARY;
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SEQUENCE FROM N.A.
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Q7W200;
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RESULT 13

[2] SEQUENCE FROM N.A. STRAIN=Bristol N2;

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Gaps

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140 AA; 15881 MW; 01DB8822ACE9F1BC CRC64;

SEQUENCE

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Control of the Embi-General Control of the Embi-General Control of the Embi-General Complex (TML-COMPLEX) and the Complex of the Embi-General Complex (COMPLEX (COMPLEX III OR CYTCCHROME B.C.I COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHATIS (BY SIMILARITY) and EMBI-COMPLEX (COMPLEX III OR CYTCHROME B.C.I COMPLEX D.C.I COUPLED TO ATP SYNTHATIS (BY SIMILARITY) (BY SIMILARITY) (COUPLED TO THE PROTEIN (BY SIMILARITY) (COMPLEX B.C.I COMPLEX B.C.I COMPLEX B.C.I COMPLEX B.C.I CYTCCHROME B.C.I STMILARITY) (COMPLEX B.C.I CYTCCHROME B.C.I CYTCCHROME B.C.I CYTCCHROME B.C.I CYTCCHROME B.C.I CYTCCHROME B.C.I CYTCCHROME B.C.I CAL4964.1; TO THE CYTCCHROME B.FAMILY.

BENDI, AJ318506; CAC44964.1; TO THE CYTCCHROME B.FAMILY.

GO; GO:0016621; C:integral to membrane; IEA.

GO; GO:0016611; F:oxidor-caductase activity; IEA.

GO; GO:0016612; C:integral C.C.II LANDER C.C.I LANDER C.C
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MEDLINE-22825697; PubMed=12917641;
Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
Lamerdin J., Regala W., Allen B.E., McCarren J., Paulsen I.,
Dufresne A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a motile marine Synechococcus.";
Mature 424:1037-1042(2001).

EMBL; BX569694; CAE08610.1; -.
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                                                                                                                                                                          Synechococcus gr. (strain WH8102).
Bacteria, Cyanobacteria; Chrococcales; Synechococcus.
NCBI_TaxID=84588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribosomal protein; Complete proteome.
SEQUENCE 86 AA; 9537 MW; 9B8BEA9CC2EE34B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Putative cytochrome b (Fragment).
                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
50S ribosomal protein L31.
RPL31, RPME OR SYNW2095.
                         86 AA.
                         PRT;
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nes 6; Conservative
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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NON TER
                                                Q7U4H3;
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                      Q7U4H3
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Q7U4H3
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Submitted (UTL-2001) to the EMBL/GenBank/DDBJ databases.

COMPLEX (COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERALES AN ELECTRCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SINILARITY)

COUPLED TO ATP ROWING (BY SINILARITY)

COUPLED TO THE RESERVE PROFIEN (BY SINILARITY)

COUPLED TO THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROFIEN (BY SINILARITY)

COUPLED TO AND THE RIESKE PROFIEN (BY SINILARITY)

COUPLED TO THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE CYTOCHROME B FAMILY.

BEMBL; AJ318501; CAC44960.1; -

COUPLED TO ATP SYNTHESIS (BY SINILARITY)

COUPLED TO THE PROFIENT OF MEMBLE BEAUTY (CHAIN; TEA.

COUPLED TO THE PROFIENT OF MEMBLE BEAUTY (CHAIN; TEA.

COUPLED TO THE PROFIENT OF THE CYTOCHROME B,
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Acidithiobacillaceae; Acidithiobacillus.
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Score 43, DB 2, Length 140, Pred, No. 19, 3, Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Putative cytochrome b (Fragment).
CYTB OR PETB2.
Thiobacillus ferrooxidans.
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          Query Match
Best Local Similarity 60.0%;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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ABU60847
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Gapop 10.0 , Gapext 0.5
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11: geneseqp1980s:*
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Aag62531 Human CRH Abu60843 Pepride p Abu60847 Pepride p Abu60847 Pepride p Adx71228 Human ppp 92 Adw31392 Human ppp 93 Adw31392 Human cxy Aag62532 Human cxy Aag62532 Human CXH Abu60844 Pepride p Adw31392 Human CXH Abu60844 Pepride p Adw31392 Human CXH Adg6253 Human CXH Adw31390 Human CXH Adw31390 Human CXH Adw31390 Human CXH Adw31370 Bovine G Adw95185 Bovine pi Adw95185 Bovine pi	GNMENTS				diagnosis, prolactin secretion; entral nervous system; pancreatic.		amide"								i t		lonal antibody which has a specific of the C-terminal of 1992 ligand or its in be used in diagnosis or to treat or the abnormality in the pituitary function motion of prolactin secretion), central and pancreatic function regulatory immunoassay can also be applied in unctions of the ligand and its derivative int peptide fragments of the 1992 ligand
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ed. No. 3.3e-06; Mismatches 0;

Pred.

100.08; 71

Local Similarity 100. nes 13; Conservative

Best Loc Matches

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AAW97236 standard; peptide; 20

RESULT 3 AAW97236

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This sequence represents a peptide fragment from a novel human type ligand polypeptide corresponding to amino acid residues 34 to 53 of the sequence represented in AMM1390 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaccutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, clizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hypercholesterolaemia, hyperglyceridaemia, hypercholaesterolaemia, hyperglyceridaemia, hyperprotactinaemia, asthma, cancer, panoreatitis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinal plantia, hyperglycardial infarction, infertility, spinal consensed in also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein
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                                                                                                                                                                                                                                                                                                                                      G protein-coupled receptor; ligand binding; pharmaceutical; modulator; pituitary; central nervous system; pancreas; prophylactic; therapeutic agent.
                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Habata Y, Kawamata Y, Hosoya M, Fujii R, Fukusumi S;
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                                  Length 14;
                                                               0; Indels
                                                                                                                                                                                                                                                                                                       Human type G protein-coupled receptor ligand fragment 4.
                              100.0%; Score 76; DB 3; I
100.0%; Pred. No. 2.2e-06;
                                                               Mismatches
                                                                                                                                                                                                             AAW31394 standard; peptide; 20 AA
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96JP-00059419.
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                                                                                                                1 TPDINPAWYASRG 13
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N-PSDB; AAV02431.
                         Query Match
Best Local Similarity
 Sequence 14 AA;
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15-MAR-1996;
12-AUG-1996;
18-SEP-1996;
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The present sequence represents a human type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing thypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for promoting plutiary adenomatosis, secretion can be used for treating or preventing plutiary adenomatosis, infertility, impotence, amenorates, galactorrhea, acromegaly, Chiarifrommel syndrome, Argonz del Castilo syndrome, Forbes-Albright syndrome, C lymphoma, Sheehan syndrome or dyszoospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function can be used for treating or preventing choriocarcinoma, hydatid mole, irruption mole, abortion, unthrifty fetus, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia
                                                                                                                                   Rat type ligand; modulation; prolactin secretion; G protein-coupled receptor; GPCF, hypovarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pituitary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorathes; galactorathea; acromegaly, Chiari-Frommel Syndrome; Argonz-del Castilo syndrome; Porbes-Albright syndrome; lymphoma; Sheehan syndrome; dyscospermia; contraceptive; placentral function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy.
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Pred. No. 3.3e-06;
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                                                                                                 Human type ligand polypeptide fragment.
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                   AAW97236;
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Sequence 20 AA;

Matches

6 원 RESULT AAY4929

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This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of furges for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                          Human, oxytocin secretion promoter, G protein-coupled receptor protein, treatment, disease, pain, atonic bleeding, uterine recovery failure, cow, caesarean section, artificial fertilization, galactostasis, goat, plg, veterinary medicine, milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                              Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl, maleimido group, amino, hydroxyl, thiol; hormone, growth factor, neurotransmitter.
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Pred. No. 3.3e-06;
Mismatches 0; Indels
           Human oxytocin secretion promoting peptide SEQ ID NO: 35.
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 19P2 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with abnormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central mervous regulatory mechanism, and pancreatic function regulatory mechanism entibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAX49290-302 represent peptide fragments of the 19P2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality.
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 Gaps
                                                                                                                                                                                                                                                                                                           Monoclonal antibody, 19P2 ligand, diagnosis, prolactin secretion, pituitary, regulatory mechanism; central nervous system; pancreatic.
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/note= "C-terminal amide"
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                                                                                                                                                                 AAY49294 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                              19P2 ligand peptide fragment
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Best Local Similarity 1000.
The 13; Conservative
                                                                                                                                                                                                                                         (first entry)
                                                                  1 TPDINPAWYASRG 13
   13; Conservative
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                                      1 TPDINPAWYASRG
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Modified-site
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RESULT 5 AAB10365

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Use of G protein receptor ligand or peptide for controlling corticotropin
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PRRP; GPRLO; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
anticonvulsant.
                                                                                                                                                                                                 The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hypercortisism, Addison's hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or
                                                                                                                                                                                                                                                                                                                             disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 76; DB 4; Length 20
100.0%; Pred. No. 3.3e-06;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE26404 standard; peptide; 20 AA.
                                                                                                                                                        Claim 4; Page 75; 90pp; Japanese.
           Hinuma
                                                                                                                   releasing hormone secretion.
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           Matsumoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-355552/37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CIVE/) CIVELLI O. (LINS/) LIN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002037533-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 AA;
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           Kitada C,
                                                                                                                                                                                                                                                                                                                                                                                                  invention
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comprising a therapeutically active amino acid region (III) and a

leastive group (II) (e.g. succinimidyl and matehindo groups) attached to

a less therapeutically active amino acid region (IV), which covalently

bonds with amino/hydroxyl/thiol groups on blood components to form a

peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth

factors and neurotransmitters, to protect them from peptidase activity in

vivo for the treatment of various disorders. Endogenous therapeutic

peptides are not suitable as drug candidates as they require frequent

administration due to rapid degradation by peptidases in the body.

Modifying and attaching therapeutic peptides to albumin prevents or

reduces the action of peptidases to increase length of activity (half

ilfe) and specificity as bonding to large molecules decreases

intracellular uptake and interference with physiological processes.

ABB90829 to AAB92441 represent peptides wich by used in the

exemplification of the present invention
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                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
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                                                                                                                                                                          Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 76; DB 4; Length 20; 100.0%; Pred. No. 3.3e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CRH releasing protein related peptide SEQ ID NO: 35.
                                                                                                                                                                          Holmes DL,
                                                                                                                                                                                                                                                                                                                       Disclosure; Page 244; 733pp; English.
                                                                                                                                                                          Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG62534 standard; peptide; 20 AA
17-MAY-2000; 2000WO-US013576.
                                                               99US-0153406P
                                             99US-0134406P
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                                                                                                                            (CONJ-) CONJUCHEM INC.
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                                           17-MAY-1999;
                                                               10-SEP-1999;
                                                                                    15-OCT-1999;
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                                                                                                                                                                     Bridon DP,
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Matches

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RESULT 7

The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PrRP) receptor (GPRIO)

Disclosure; Page 25; 35pp; English.

18-NOV-1999; 99JP-00327900. 26-SEP-2000; 2000JP-00297073. 17-NOV-2000; 2000WO-JP008119.

18-NOV-1999;

(TAKE ) TAKEDA CHEM IND LTD.

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Gaps ö

Length 20;

Gaps

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Indels

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Mismatches

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Conservative

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agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. Prep receptor agonists may be used to treat common disorders which lead to sleepiness, e.g. sleep apnocea, narcolepsy, idiopathic hypersomnia and psychogenic hypersomnia. PrRp receptor antagonists are useful for disorder and psychophysiologic insomnia such as adjustment sleep disorder and psychophysiologic insomnia. The present sequence is human PRRP-31 C-terminal peptide, PrRP-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 3.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU60846 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2001; 2001JP-00147341.
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Best Local Similarity 100.
Matches 13; Conservative
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gene recombination.
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                                                                                                                                                                                                                                   Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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ABU60846
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Length 20;

Score 76; DB 6; Pred. No. 3.3e-06;

100.0%; 100.0%;

Query Match Best Local Similarity

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This sequence represents a peptide fragment from a novel human type [1] gand polypeptide corresponding to amino acid residues 34 to 54 of the sequence represented in AAW13190 and is used in an assay to monitor [1] igand binding to the G protein-coupled receptor protein. Pharmaceutical isomositions containing this ligand may be used as a pituitary function compositions central nervous system medulator or a paracreatic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, cor disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, prince, schizophrenia, trauma, concertisis, arenal disease, Turner's syndrome, neurosis, asthma, concertisis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinal and egeneration, bone fracture, trauma, atopic dermatitis, spinal and or screen compounds which are capable of altering the binding activity of the compounds which are capable of altering the binding activity of the compounds which are capable of altering the binding activity of the compounds spinal activation of the G protein-coupled receptor protein
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pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
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100.0%; Pred. No. 3.5e-06;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                               Human type G protein-coupled receptor ligand fragment 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawamata Y,
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96JP-00059419.
96JP-00211805.
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                                                                                                                   AAW31395 standard; peptide;
                                                                                                                                                                                   (first entry)
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Matches 13; Conservative
13
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1 TPDINPAWYASRG
                               TPDINPAWYASRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAKE ) TAKEDA
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15-MAR-1996;
12-AUG-1996;
18-SEP-1996;
                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     WO9724436-A2
                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-1996;
                                                                                                                                                                                   06-APR-1998
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                                                                                                                                                   AAW31395;
                                                                                   RESULT 10
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                                                                                                                                                                                                             Human, oxytocin secretion promoter, G protein-coupled receptor protein, treatment, disease, pain, atonic bleeding, uterine recovery failure, cow, caesarean section, artificial fertilization, galactostasis, goat, pig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 76; DB 3; Length 21; 100.0%; Pred. No. 3.5e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                   Human oxytocin secretion promoting peptide SEQ ID NO: 36.
                                                                                                                                                                                                                                                              veterinary medicine, milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 63; 72pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hinuma
                                                                                         AAB10366 standard; peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                  99WO-JP007199
                                                                                                                                                     (first entry)
TPDINPAWYASRG 13
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                                                                                                                                                     24-NOV-2000
                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsumoto H,
                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1999;
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AAG62535
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AC AAG62
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AC AAG62
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DT 24-AU
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DE Human
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Human CRH releasing protein related peptide SEQ ID NO: 36.

(first entry)

24-AUG-2001

AAG62535;

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                                                                                                                                                                                                                                                                                                      Use of G protein receptor ligand or peptide for controlling corticotropin
                                                                                                                                                                                                                                                                                                                                                                    The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nausea, pigmentation, hypogonadism, hair loss, and hypotensically adrenal gland hypotunction and obesity. The present sequence is a peptide used in the exemplification of the
Human, corticotrophin releasing hormone, CRH; G protein receptor ligand,
analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism;
Addison's disease; adrenal gland hyperfunction; obesity.
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100.0%; Pred. No. 3.5e-06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                               Hinuma
                                                                                                                                          17-NOV-2000; 2000WO-JP008119.
                                                                                                                                                                      18-NOV-1999; 99JP-00327900.
26-SEP-2000; 2000JP-00297073
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                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                     releasing hormone secretion
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                                                                                   WO200135984-A1
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                                                                                                               25-MAY-2001
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                                                                                                                                                                                                                                            Kitada C,
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The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptide e.g. KiSS-1 peptide and GPRB ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
                                                       Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g protein-coupled receptor; ligand binding; pharmaceutical; modulator;
pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland.
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                                                                                                                                                                                                                                                                                                                                 Length 21;
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human type G protein-coupled receptor ligand fragment 6.
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Kitada C;
                                                                                                               Disclosure; Page 69; 87pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawamata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 186; 258pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW31396 standard; peptide; 22 AA.
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96JP-00059419.
96JP-00211805.
96JP-00246573.
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                                                                                                                                                                                                                                                                                                                                                                                           1 TPDINPAWYASRG 13
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 Suenaga M,
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                              WPI; 2003-129302/12.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapeutic agent
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                                                                                                                                                                                                                                                                                                       Sequence 21 AA;
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12-AUG-1996;
18-SEP-1996;
 Nishimura O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Kitada
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This sequence represents a peptide fragment from a novel human

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ligand polypeptide corresponding to amino acid residues 34 to 55 of the sequence represented in AMM3139 and is used in an assay to monitor or ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator. This ligand could have, specific applications as a prophylactic or therapeutic agent for dementa, depression, hyperkinetic syndrome, or therapeutic agent for dementa, applications as a prophylactic or therapeutic agent for dementa, appression, hyperkinetic syndrome, correctly disease, hyper and polyphagia, hyperlipidaemia, hypertholesterolaemia, hyperalyseridaemia, hypercolactinaemia, trauma, crancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, concer, pancreatitis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinal and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the compounds which are capable of altering the binding activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
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100.0%; Pred. No. 3.7e-06;
iive 0; Mismatches 0;
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 AA;
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medicine for promoting milk production in cow, goat and pig. This sequence represents a human peptide which acts as an oxytocin secretion promoter
                                                                                                                                          Query Match
Best Local Similarity 100.0%; Score 76; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                    Sequence 22 AA;
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Search completed: August 12, 2004, 14:43:54 Job time: 27.7122 secs

1 TPDINPAWYASRG 13 |||||||||||| 1 TPDINPAWYASRG 13

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Sequence 28, P Sequence 38, P Sequence 82, P Sequence 84, P

Sequence

Sequence 86, Appl Sequence 17, Appl Sequence 17, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 16, Appl Sequence 11, Appl Sequence 11, Appl Sequence 96, Appl Sequence 94, Appl Sequence 197, Appl Sequence 1983, Appl Sequence 1983, Appl Sequence 1984, Appl Sequence 1094, Appl Sequence 288980, Sequence 288980,

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Sequence 18, Application US/09932161
Fatent No. US2002037533A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Civelli, Olivier
APPLICANT: Civelli, Olivier
APPLICANT: Civelli, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2000-04-128
FRIOR APPLICATION NUMBER: US 09/560,915
FRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
13 US-10-096-777-13
13 US-10-044-592-40
13 US-10-044-592-40
13 US-10-044-592-28
13 US-10-044-592-86
13 US-10-044-592-86
13 US-10-044-592-86
13 US-10-044-592-86
14 US-10-044-592-86
15 US-10-044-592-86
16 US-10-044-592-86
17 US-10-092-11-14
18 US-10-094-592-96
18 US-10-437-963-993-680-925-299-1094
18 US-10-424-599-248980
2 US-10-424-599-248980
2 US-10-389-647-469
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100.0%; Pred. No. 3.3e-05;
iive 0; Mismatches 0;
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Sequence 18, Application US/10096777
Publication No. US20030171270A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Steven
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Matches 13; Conservative
  CRGANISM: Homo Sapien
US-09-932-161-18
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    Query Match
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Sequence 27, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 14, Appl
Sequence 78, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 39, Appl
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Sequence 18, Appl
                                                                                           August 12, 2004, 14:49:10 ; Search time 22.9767 Seconds (without alignments) 177.617 Million cell updates/sec
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Sequence 15, 7
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-096-777-18

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US-10-044-592-27

US-10-044-592-27

US-10-044-592-42

US-10-044-592-43

US-10-044-592-43

US-10-044-592-78

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US-10-044-592-26

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                              US-09-700-643A-2_COPY_12_24
76
1 TPDINPAWYASRG 13
                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Sequence 27, Application US/10044592

Sequence 27, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:
APPLICANT: Fitusumi, Shuji
APPLICANT: Fitusumi, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT FILING DATE: 2002-01-10
PRIOR FILING DATE: 1999-25-10

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1999-04-27

PRIOR FILING DATE: 1997-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE:
SOFTWARE
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VESUUT:

VESUUT:

Sequence 92, Application US/10044592

Sequence 92, Application US/10044592

Sequence 92, Application US/10044592

Publication.No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

APPLICANT: Hinuma, Shuji

APPLICANT: Hinuma, Shuji

APPLICANT: Hinuma, Shuji

CURRENT HILION POLYPEPTIGES, their Production and Use

FILE REFERENCE: 2463US2P

CURRENT FILING DATE: 2002-01-10

PRIOR PILING DATE: 1999-25-10

PRIOR FILING DATE: 1999-6-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1998-04-27

PRIOR FILING DATE: 1997-04-28

SOFTWARE:

SOFTWARE:

SEQ ID NO 92

LENGTH: 87

TYPE: PRI

CREATH: 87

CREATH: 87
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100.0%; Score 76; DB 13;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                    100.0%; Score 76; DB 14; 100.0%; Pred. No. 5.1e-05;
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Best Local Similarity 100.
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                      1 TPDINPAWYASRG 13
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                                                    ) ORGANISM: Homo Sapien
US-10-096-777-15
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US-10-096-777-15
Sequence 15, Application US/10096777
Publication No. US20030171270A1
SEQUENCE 15 IN PERMITTON:
HERBERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: US/05/560,915
PRIOR PILING DATE: 2000-04-28
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TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
PRIOR PILIATION NUMBER: US/09/560,915
PRIOR PILIATION NUMBER: US/09/560,915
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 20
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Patent No. US20020037533A1

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

APPLICANT: Lin, Steven

TITLE OF INVENTION: Screening and Therapeutic Methods For
TITLE OF INVENTION: Promoting Wakefulness and Sleep

FILE REFERENCE: P-UC 4679

CURRENT APPLICATION UNBER: US/09/932,161

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION UNBER: US 09/560,915

PRIOR APPLICATION NUMBER: US 09/560,915

NUMBER OF SEQ ID NOS: 24

NUMBER OF SEQ ID NOS: 24
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100.0%; Score 76; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 31
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; ORGANISM: Homo Sapien
US-10-096-777-18
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; ORGANISM: Homo Sapien
US-09-932-161-15
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US-10-096-777-16

Sequence 16, Application US/10096777

Publication No. US20030171270A1

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

APPLICANT: Civelli, Olivier

APPLICANT: Civelli, Steven

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PTRP)

TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PTRP)

CURRENT APPLICATION NUMBER: US/10/096,777

CURRENT FILING DATE: 2002-03-12

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16

LENGTH: 20

TYPE: PRT
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| Sequence 44, Application US/10044592
| Publication No. US20020143152A1
| GENERAL INFORMATION:
| APPLICANT: Hinuma, Shuji
| APPLICANT: FURNEUM; Shoji
| TITLE OF INVENTION: Polypeptides, their Production and Use
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Matches 12; Conservative
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US-10-096-777-16
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                             0; Gaps
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APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shoji
TITLE OF TEXASURION NOWBER: US/10/044,592
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER: OF SEQ ID NOS: 96
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94.7%; Score 72; DB 9; Length 20;
Best Local Similarity 92.3%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 1; Indels
Best Local Similarity 92.3%; Pred. No. 0.00014;
Matches 12; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lin, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For
TITLE OF INVENTION: Screening wakefulness and Sleep
FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastesQ for Windows Version 4.0
                                                                                                                                                                                                                                              Sequence 16, Application US/09932161
Patent No. US20020037333A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-044-592-42
, Sequence 42, Application US/10044592
, Publication No. US20020143152A1
, GENERAL INFORMATION:
                                                                          1 TPDINPAWYASRG 13
                                                                                                                     1 TPDINPAWYAGRG 13
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Best Local Similarity 92.3;
Matches 12; Conservative
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US-09-932-161-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bovine
                                                                                                                                                                                                                             US-09-932-161-16
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LENGTH: 20
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SEQ ID NO 42
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                            TITLE OF INVENTION: Polypeptides, their Production and Use FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US,10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1998-64-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1997-04-28

NUMBER OF SEQ ID NOS: 96
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US-09-321-161-13

Sequence 13. Application US/09932161

Parent No. US20020037533A1

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

TITLE OF INVENTION: Screening and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep

FILE REPERBNCE: P-UC 4679

CURRENT APPLICATION NUMBER: US/09/932,161

CURRENT PILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 09/560,915

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 31
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Pred, No. 0.00021;
0; Mismatches 1; Indels
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Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinna, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use; FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
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Best Local Similarity 92.33;
Thea 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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US-09-932-161-13
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LENGTH: 29
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Sequence 78, Application US/10044592

Publication No. US20020143152A1

GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION: Polyeptides, their Production and Use
FILE REFERENCE: 2463US2P
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR PILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE:
SEQ ID NO 78

LENGTH. 25
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Pred. No. 0.00016;
0; Mismatches 1; Indels
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PILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR PILING DATE: 1998-04-27
PRIOR PILING DATE: 1998-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE: SOFTWARE: 1997-04-28
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US-10-044-592-26
Sequence 26, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
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Best Local Similarity 92.3%;
Matches 12; Conservative (
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NAMBE/KEY: misc feature
LOCATION: (1)...(20)
COTHER INFORMATION: primer
LOCATION: (52)...(76)
COTHER INFORMATION: primer
US-10-044-592-78
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPDINPAWYASRG 13
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Best Local Similarity
Thes 12; Conservat
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; ORGANISM: Bovine
US-10-044-592-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 25
TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-10-044-592-78
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CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923

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sequence 34, Appl sequence 34, Appl sequence 16, Appl sequence 35, Appl sequence 36, Appl sequence 10, Appl sequence 29, Appl sequence 29, Appl sequence 29, Appl sequence 31, Appl sequence 31, Appl sequence 31, Appli sequence 31, Appli
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 46, Application US/09105678A
; Sequence 46, Application US/09105678A
; Patent No. 610386Z
; General Information:
    APPLICANT: Suenaga, Masato
    APPLICANT: Tanaka, Takeo
    APPLICANT: Tanaka, Yoko
    APPLICANT: Nishimura, Osamu
    TILLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
    NUMBER OF SEQUENCES: 52
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
    STREET: 130 Water Street
    CITY: Boston
    STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
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MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPUTER: TEM PC COMPUTER: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
RILING DATE: 26-JUN-199
ATTORNEY/AGENT INFORMATION:
NAME: COMIST, DAVIG G
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION INFORMATION:
TELEPHONE: 617-523-3400
THELEPAX: 617-523-3400
THELEPAX: 617-523-3400
THELEPAX: 617-523-3400
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100.0%; Score 76; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 13; Conservative 0; Mismatches 0;
US-09-421-208-30
US-09-105-678A-34
US-08-776-971-98
US-09-560-915-16
US-09-105-678A-35
US-09-105-678A-35
US-09-105-678A-35
US-09-105-678A-36
US-09-105-678A-36
US-09-105-678A-36
US-09-105-678A-36
US-09-105-678A-29
US-09-105-678A-29
US-09-776-971-11
US-09-776-971-11
US-09-776-971-3
US-09-776-971-3
US-09-105-678A-29
US-09-105-678A-29
US-09-105-678A-31
US-09-105-678A-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 20 amino acids amino acid
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     TOPOLOGY: linear
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US-09-105-678A-46
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-476-971-64
US-09-650-915-18
US-09-105-678A-47
US-09-105-678A-47
US-09-105-678A-48
US-09-105-678A-48
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US-09-105-678A-48
US-09-105-678A-48
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US-09-105-678A-9
US-09-105-678A-9
US-09-105-678A-45
US-08-176-971-135
US-08-176-971-138
US-08-176-971-138
US-08-176-971-138
US-08-176-971-138
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                                                                                  - protein search, using sw model
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76
1 TPDINPAWYASRG 13
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      August 12, 2004, 14:37:36
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Perfect score:
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Maximum DB seq
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                                                                                                                      Run on:
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No.
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USA
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STATE: MA
COUNTRY: US/
ZIP: 02109
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Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Xitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
COUNTRY: USA
ZIP: O2109
COMPUTER: EABABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
COMPUTER: IBM COMPATER: DS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION NATE: US/08/776,9718
FILING DATE: 06-Feb-1997
APPLICATION NATE: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/21805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/21805
ATTORNEY/AGENT INFORMATION:
NAME: COALLIN, DAVId G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-08-776-971-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPAN: 617-523-5440
INPORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                           Sequence 64, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
US-08-776-971-64
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Sequence 200 Septication US/09421208
Sequence 200 Septication US/09421208
Sequence 200 Septication US/09421208
SepticANT: Suenga Meach
APPLICANT: Mankay Yoke
APPLICANT: Mankay Yoke
APPLICANT: Mankay Yoke
CONDESCEDE DIVER MENDORPHY & CUSHWAN, LLP
STREET 10 Water Street
CTTY: Beach
CTTY: Beach
CTTY: Beach
CTTY: Beach
CONDESCEDE DIVER MENDORPHY & CUSHWAN, LLP
STRIET 10 Water Street
CTTY: Beach
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RESULT 3

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Hosoya, Masaki
Fujii, Ryo
Fudiai, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Patent No. 6288561
GENERAL INFORMATION:
APPLICANT: Suemaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoke
APPLICANT: Tanaka, Yokeo
APPLICANT: Mishimura, Osamu
ITILE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFFWARE: FastSEM for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFTCATION ATA:
APPLICATION ATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 12-MG-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AG-1996
APPLICATION NUMBER: JP 8/2165
APPLICATION NUMBER: JP 8/2165
ATTORNEY AGENT INPORMATION:
MAME: CONLIN, DAVIG G.
REFERENCE/DOCKET NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-08-776-971-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPDINPAWYASRG 13
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                                                              Query Match 100.0%; Score 76; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 1.3e-06; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47, Application US/09105678A
| Patent No. 6103882
| GENERAL INFORMATION:
| APPLICANT: Stenaga, Masato | APPLICANT: APPLICANT: APPLICANT: Moriya, Takeo | APPLICANT: Nishimura, Osamu | TILLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND | NUMBER OF SEQUENCES: 52 | CORRESPONDENCE ADDRESS: 10 Number OF SEQUENCES: 52 | CORRESPONDENCE ADDRESS: 10 Number OF SEQUENCES: 53 | CORRESPONDENCE ADDRESS: 10 Number OF SEQUENCES: 53 | CORRESPONDENCE ADDRESS: 10 Number OF SEQUENCES: 53 | CONTRESSEE: 10 Number OF SEQUENCES: 53 | CONTRESSEE: NA COUNTRY: USA | COUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentur Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INPORMATION:
NAME: CONLIN, David G:
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION INPORMATION:
TELEPKN: 617-523-640
INPORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 2014
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100.0%; Score 76; DB 3; L
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 13; Conservative 0; Mismatches 0;
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Setent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                         1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                       1 TPDINPAWYASRG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
US-09-560-915-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-08-776-971-65
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NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REPRENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEFRONE: 677-523-340
TELEFAX: 617-523-340
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 66, Application US/08776971B; Patent No. 6228984; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                          LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-48
                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-776-971-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 76; DB 3; Length 21; 100.0%; Pred. No. 1.4e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 48, Application US/09105678A

Patent No. 610382

CENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Niethmura, Osamu
TITLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: USA CATOLOGY CONTY; USA CATOLOGY COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPOTHER: IBM PC COMPATIBLE COMPOTHE: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: CA-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TO 172118/1997
ATTORNEY/AGENT INFORMATION:
                                                                                                         COMPUTER READABLE FORM:
MBIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REFRENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 47: SEQUENCE CHARACTERISTICS: LENGTH: 21 amino acids
       130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: peptide US-09-421-208-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                   USA
                            Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                 COUNTRY: UK
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-105-678A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-09-105
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APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Habata, Yuji
Hasaya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSER: 1140
STREET: 1130 Water Street
                                                                        .
0
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDION TYPE: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FastESD for Windows Version 2.0
SOFTWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION MUMBER: PCT/JP96(03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: DF 7/34371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JF 8/59419
FILING DATE: 15-WAR-1996
APPLICATION NUMBER: JF 8/246573
FILING DATE: 18-SEP-1996
APPLICATION NUMBER: J7 026
REGISTRATION NUMBER: 27,026
TELEPROMINICATION NUMBER: 47176
TELECOMMUNICATION NUMBER: 47176
TELECOMMUNICATION NUMBER: 47176
TELECOMMUNICATION NUMBER: 37,026
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Fatent No. 6258561
GENERAL INFORMATION:
APPLICANT: Society Takeo
APPLICANT: Anaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 76; DB 3; L
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
APPLICATION NUMBER: UP 1/2118/1997
FILING DATE: 27-UN-1997
ATTONNEY/AGENT INFORMATION:
NAME: CONLIN, DAVIG G.
REGISTANTION NUMBER: 48466-342
REGISTANTION NUMBER: 48466-342
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
TOWNSTRIPE OF AMERICA INFORMATION FOR SEQ 1D NO: 48:
                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-08-776-971-66
                      LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                           1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYASRG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
COUNTRY: US.
ZIP: 02109
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Pred. No. 2.2e-06;
0; Mismatches 0; Indels
                                    Sequence 9, Application US/09105678A

Patent No. 6103882

GENERAL INFORMATION:
APPLICANT: Such as a second a septicant of a septicant anaka, Yoko
APPLICANT: Tanaka, Yoko
CARESPONDENCE SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Guanaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 23.3400
TELEPHONE: 617-523-6440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
THATCH FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.'
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                           STREET: 130 WE
CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
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US-09-105-678A-43
RESULT 11
US-09-105-678A-9
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Sequence 9, Application US/09421208
; Patent No. 629851
; GENERAL INFORMATION:
; APPLICANT: Suenas Masato
APPLICANT: Tanaka, Yoko
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 5.2
CORRESPONDENCE ADDRESS:
; ADDRESSEB: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
; CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 76; DB 3; Length 31 Best Local Similarity 100.0%; Pred. No. 2.2e-06; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 47176
REFERENCE/DOCKET NUMBER: 47176
TELEPRONEY 17-523-3400
TELEPAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
TENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRICK APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY AGENT INFORMATION:
NAME: CONLIN, David G.
REGISTATION NUMBER: 27,026
REFERENCE/POCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 31 amino acids
IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPDINPAWYASRG 13
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Kawamata, Yugo
Kawamata, Yugo
Kawamata, Yugo
Kawamata, Yugo
Fujii, Mooya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 76; DB 3; Length 31; Best Local Similarity 100.0%; Pred. No. 2.2e-06; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
ODERATING SYSTEM: DOS
SOFTWARE: FASTSEC for Windows Version. 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION AUTOMAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1996
                ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,678A

FILING DATE: 27-JUN-1998

PRIOR APPLICATION NUMBER: JP 172118/1997

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: COALIN, David G.

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELEFONE: 617-523-3400

TELEFAK: 617-523-3400

INPORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 61, Application US/08776971B
Patent No. 6228984
GENERAL INPORMATION:
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 TPDINPAWYASRG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
COUNTRY: USA
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US-08-776-971-61
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US-09-421-208-43

US-09-421-208-43

Sequence 43. Application US/09421208

Patent No. 625861

Sequence 43. Application US/09421208

Patent No. 625861

September Second Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yakeo

APPLICANT: Tanaka, Yakeo

APPLICANT: Moriya, Takeo

APPLICANT: Mishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDER ADDRESS:

ADDRESSED: DIKE, BRONSTEIN, ROBERTS & CUSHWAN, LLP

STRAET: 130 Water Street

CITY: BRONSTEIN, ROBERTS & CUSHWAN, LLP

STRAET: MA

COUNTRY: READABLE FORM:

MEDIUM TYPE: PLOPS/Mb-DOS

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/Mb-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-UN-1998

APPLICATION NUMBER: US 09/105,678

FILING DATE: 27-UN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Conlin, David C

RESERRICE/DOCKET NUMBER: 48466-342

TELERRONG POSTERISTICS:

LENGTH: 31 anino acids

"WERE THING DATE: 100 A 31: 10
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                                                                                                                                                                                                             Query Match
100.0%; Score 76; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   1 TPDINPAWYASRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 TPDINPAWYASRG 24
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-43
                                                                         TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-421-208-9
TYPE: amino acid STRANDEDNESS:
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Search completed: August 12, 2004, 14:52:13 Job time: 7.40698 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 14:37:36; Search time 5.74419 Seconds

(without alignments)
217.697 Million cell updates/sec

Title: US-09-700-643A-3_COPY_12_24

Perfect score: 79
Sequence: 1 TPDINPAWYTGRG 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366
```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : 'PIR 78:*
1: pir1:*

.abase : 'PIR 78:*
1: Dirl:*
2: Dir2:*
3: Dir3:*
4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	prolactin-releasin	cal	hypothetical prote	_	RVS167 protein - y	hypothetical prote	protein C34G6.7 [i		Grb-2 related adap		beta-glucosidase h	beta-glucosidase h	endo-xyloglucan tr	xyloglucan endo-1,	related to trichod	hepatocyte growth	gene 30 protein -	hypothetical prote	excinuclease ABC c	hypothetical prote	amir	probable inner mem	inner membrane tra	⊐	ase	excinuclease ABC c	excinuclease ABC c	excision nuclease	
SUMMAKIES	UC7607	H84384	T33175	T21969	40887	.84780	G87789	T47548	JE0376	B69009	109021	T09022	51754	161555	51214	30811	30975	B72621	67485	09373	164720	G90629	G85480	T33732	A64608	H96961	BVECUA	H91258	
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Length D	83	139	527	167	482	398	449	4	ന	430	498	517	120	269	529	1425	101	126	280	395	476	476	476	925	935	939	940	940	1
% Query Match	100.0	58.2	58.2	57.0	ġ	'n	55.7	55.7	54.4	54.4	54.4	54.4	ო	53.2	m.	ო	ä	ä	51.9	51,9	51.9	Η.	51.9	Η.	51.9	51.9	51.9	51.9	
Score	79	46	46	45	44.5	44		44	43	43	43	43	42	42	42	42	41	41	41	41	41	41	41	4.1	41	41	41	41	
Result No.		N	m	4	ľ	9	7	α	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	

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D86099 E71906	11 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	B81454	AE1017	D64057	F95021	C97893	E83117	AF0040	B81883	H89848	A81138	T46550	D71645	F97861	AB1761
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51.9	0.5	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9
	- -	41	41	41	41	41	41	41	41	41	41	41	41	41	41
44															

## ALIGNMENTS

1 TPDINPAWYIGRG 13 1 TPDINPAWYIGRG 13 1 TPDINPAWYIGRG 13 1 TPDINPAWYIGRG 45 13 TPDINPAWYIGRG 45 14	Ouery Match Best Local Similarity 10 Matches 13; Conservativ	A,Contents: Spleen A,Contents: Spleen A,Molecule type: DNA A,Molecule type: DNA A,Residues: 1-83 < YAM> A,Residues: 1-83 < YAM> C,Comment: This peptide induces arachidonic acid metabolite release from rat anterior pi release, and stimulation of ACTH secretion from the pitultary. C,Genetics: A,Gene: PRP A,Introns: 33/1	RESULT 1 JC7607  prolactin-releasing peptide - rat prolactin-releasing peptide - rat prolactin-releasing peptide - rat prolactin-releasing peptide - rat C;Space: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001 C;Accession: JC7607 R;Yamada, M.; Ozawa, A.; Ishii. 28.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T. Biochem: Blophys: Res. Commun. 281, 53-55, 2001 A;Title: Isolation and characterization of the rat prolactin-releasing peptide gene: Mul A;Reference number: JC7607; MUID:21092785; PMID:11178959
----------------------------------------------------------------------------------------------------	--------------------------------------------------------------------	---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

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C;Date: 31-Mar-1992 #sequence_revision 06-Feb-1995 #text_change 21-Jul-2000 C;Accession: S40887; S69672 R;Bauer, F.; Urdaci, M.; Aigle, M.; Crouzet, M. Mol. Cell. Biol. 13, 5070-5084, 1993 Myl. Cell. Biol. 13, 5070-5084, 1993 A;Title: Alteration of a yeast SH3 protein leads to conditional viability with defects in A;Reference number: S40887; MUID:93330299; PMID:8336735
                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-482 <DIE>
A;Cross-references: EMBL:U32274; NID:g927313; PIDN:AAB64830.1; PID:g927321; GSPDB:GN0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypochetical protein At2g16400 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Space: O.S.Feb-2001 #sequence_revision 02-Feb-2001 #sequence_revision 02-Feb-2001 (C.S.Accession: CG4780 (C.S.Accession: CG4780 (C.S.) Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N., K., K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Mature 402, 761-768, 1999
                                                                                                                                                                                                                                                                         Ribietrich, F.S. submitted to the EMBL Data Library, July 1995
submitted to the EMBL Data Library, July 1995
A:Description: The sequence of S. cerevisiae cosmids 9481, 9509, 9926, 9461, and lambda
A:Reference number: 869665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule Vype: DN
A;Residues: 1-398 <STO>
A;Cross-references: GB:AE002093; NID:g4581140; PIDN:AAD24624.1; GSPDB:GN00139
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C;Species: Caenorhabditis elegans
C;bate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: G87789
                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-482 <BAU>
A;Cross-references: EMBL:M92092; NID:g172615; PIDN:AAA35051.1; PID:g172616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Superfamily: RVS167 protein; RVS161 protein homology; SH3 homology C.Superfamily: RVS167 protein RVS161 protein C.Keywords: transmembrane protein F;4-270/Domain: RVS161 protein homology <RVS>F;292-422/Region: alanine/glycine/proline-rich F;428-477/Domain: SH3 homology <SH3>
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Pred. No. 23;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: SGD:RVS167; MIPS:YDR388w
A;Cross-references: SGD:SO002796; MIPS:YDR388w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44;
Pred. No. 2
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Best Local Similarity 66.7%;
Matches 8; Conservative 2
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Best Local Similarity 63...
7; Conservative
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G87789
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A;Map position: 4
A;Introns: 50/2; 118/1; 139/2; 189/3; 226/1; 248/1; 287/2; 375/2; 432/3; 465/3; 548/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-27 <GRA
A;Cross-references: EMBL:AF067936; PIDN:AAC19213.1; GSPDB:GN00023; CBSP:C24G6.6
A;Experimental source: strain Bristol N2; clone C24G6
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                                                                                                                                                                                                                                                                                             hypothetical protein C24G6.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T3175
R;Greco, T.; Bradahaw, H.; Keppler, D.
Submitted to the EMBL Data Library, May 1998
A;Reference number: 221298
A;Reference number: 221298
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21969
R;Matthews, P.
                                                                   Gaps
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           h Similarity 61.5%; Pred. No. 3.8; 8; Conservative 1; Mismatches 4; Indels
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Pred. No. 14;
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A;Reference number: 219495
A;Accession: T21969
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-767 <WIL>
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840887
RVS167 protein - yeast (Saccharomyces cerevisiae)
N'Alternate names: protein YDR388w
C;Species: Saccharomyces cerevisiae
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2; Mismatches
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A.Map position: 5
A.Introns: 20/3; 77/1; 129/2; 208/3; 470/2
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Best Local Similarity 58.3%;
Matches 7; Conseryative
                                                                                                                     1 TPDINPAWYTGRG 13
                                                                                                                                                                     32 TEDITANFIGLG 44
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             Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
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Matches
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conserved hypothetical protein MTH1070 - Methanobacterium thermoautotrophicum (strain De C;Species: Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Species: Jouan-1999 #sequence_revision 29-Jan-1999 #text_change 23-Jul-1999 C;Date: 29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 23-Jul-1999 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Aju, D., Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Xi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997 Machanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Sratus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Mossiduse: 1.430 AVIII-
A;Mossiduse: 1.430 AVIII-
A;Experimental source: GB:AE000877; GB:AE000666; NID:g2622157; PIDN:AAB85559.1; PID:g262216
A;Experimental source: strain Delta H
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R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancrc Rubmitted to the Protein Sequence Database, June 1999
A;Reference number: Z16533
A;Accession: T09021
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A;Map position: 4
A;Introns: 42/3; 64/1; 80/3; 106/1; 130/1; 159/2; 244/3; 283/2; 355/3; 390/1; 420/2
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-glucosidase homolog T27E11.60 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: il-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C;Accession: T09022
Gaps
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A;Residues: 1-498 «BEV»
A;Coss-references: EMBL:AL078579; GSPDB:GN00062; ATSP:T27E11.60
A;Experimental source: cultivar Columbia; BAC clone T27E11
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Pred. No. 35;
0; Mismatches 3; Indels
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Indels
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C;Superfamily: conserved hypothetical protein MTH1070
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S4.4%; Score 43; DB

Best Local Similarity 54.5%; Pred. No. 40;

Matches 6; Conservative 3; Mismatches
Mismatches
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illarity 70.08;
Conservative
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    6; Conservative
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Best Local Similarity
                                                                                        5 NPAWYTGR
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    Matches
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Ryanonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
AyItie: Genome sequence of the nematode C. elegans: a platform for investigating biolog AyItie: Genome sequence of the nematode C. elegans: a platform for investigating biolog AyNote: see websites genome wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C elegans/ and symw sanger.ac.uk/Projects/C elegans/ AyNote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and AyStatus: preliminary
AyNote: DNA
AyNote: DNA
AyNote: DNA
AyNote: Contains similarity to an SH3 domain
C,Genetics:
A,Mor position: 1
A,Mor position: 1
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Cyperation are pure more than a finance of the second sequence revision 20-Apr-2000 #sequence S. Partamann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; Rayer, K.F.X.

Submitted to the Protein Sequence Database, April 2000
A; Reference number: Z24458
A; Recession: T47548
A; Recidues: preliminary
A; Molecule type: DNA
A; Residues: 1-548 < NYA>
A; Residues: 1-548 < 
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Clbate: 23-uul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
ClAccession: JE0376
Right, M; Hua, S; Agrawal, M; Li, G;, Cai, J;, Chan, E;, Zhou, H;, Luo, Y;, Liu, M. Right, M; Res. Commun. 253, 443-447, 1998
A;Title: Molecular cloning and expression of human Grap-2, a novel leukocyte-specific SA; Accession: JE0376
A;Accession: JE0376
A;Accession: JE0376
A;Accession: JE0376
A;Accession: JE0378
A;A
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Pred. No. 25;
2; Mismatches 3; Indels
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27;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #
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Pred. No.
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75.0%;
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Matches 7; Conserv
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RiMedford, J.I.; Elmer, J.S.; Klee, H.J.
Plant Cell 3, 359-370, 1991
A;Title: Molecular cloning and characterization of genes expressed in shoot apical merist A;Reference number: JQ1022; MUID:93005704; PMID:1840916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T51214
S.Schulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25286
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-157,'TH',160,'LESL',165,'TMSLSVSC',174,'QRT',178-182,'VRQFMERQS',191-194,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Bevan, M.; Kalicki, J.; Wohldmann, P.; Smith, A.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, August 1999
A;Reference number: Z17873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related to trichodiene oxygenase cytochrome P450 [imported] - Neurospora crassa NAALernate names: protein B44M22.100 C;Species: Neurospora crassa Crispecies: Neurospora crassa C.Species: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 16-Feb-2001
    A,Accession: S57771
A,Status: nucleic acid sequence not shown
A,Molecule type: DNA
A,Residues: 104-269 <ARR>
A,Cross-references: EMBL:X82683; NID:g576936; PIDN:CAA58001.1; PID:g576937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: endoxyloglucan transferase
C;Keywords: glycosidase; hydrolase
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-269/Product: xyloglucan endo-transglycosylase #status predicted <MAT>
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A;Map position: 6
A;Introns: 85/1; 130/1; 246/2; 391/2; 475/2
C;Superfamily: Fusarium trichodiene oxygenase 4; cytochrome P450 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M63166; NID:g166777; PIDN:AAA32828.1; PID:g166778
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F;326-493/Domain: cytochrome P450 homology <P45>
F;471/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1.529 <SCH>
A;Cross-references: EMBL:AL390354; GSPDB:GN00116; NCSP:B24M22.100
A;Experimental source: strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AL109796; GSPDB:GN00062; ATSP:F9N11.120
A;Experimental source: cultivar Columbia; BAC clone F9N11
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Pred. No. 31;
1; Mismatches
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Pred. No. 62;
0; Mismatches
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Best Local Similarity 60.0%;
Matches 6; Conservative 0
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Matches 7; Conservative
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A;Introns: 88/3; 153/2
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A, Status: preliminary
A, Molecule type: DNA
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R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancrd
submitted to the Protein Sequence Database, June 1999
A;Reference number: 216533
                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 4
A;Introns: 42/3; 64/1; 80/3; 106/1; 130/1; 159/2; 244/3; 283/2; 359/1; 367/3; 397/1; 439
C;Superfamily: Agrobacterium beta-glucosidase
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A; Rossidues: 17-269 KRAM>
A; Cross-references: EMBL: D63508; NID: g1805365; PIDN: BAA09783.1; PID: g944810
A; Note: meri5B
B; Arrowsmith, D.A.; de Silva, J.
B; Allor Biol. 28, 391-403, 1995
A; Title: Characterisation of two tomato fruit-expressed cDNAs encoding xyloglucan endo-the Reference number: S57769; NUID: 95359399; PMID: 7632911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Park, J.H.; Oh. S.A.; Kim, Y.H.; Woo, H.R.; Nam, H.G. Plant Mol. Biol. 37, 445-454, 1998 A;Title: Differential expression of senescence-associated mRNAs during leaf senescence A;Reference number: 225447; MUID:98278374; PMID:9617812 A;Accession: T51754
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T51754
endo-xyloglucan transferase [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 03-Nov-2000
C;Accession: T51754
R;Park, J.H.; Oh, S.A.; Kim, Y.H.; Woo, H.R.; Nam, H.G.
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0
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A;Cross-references: EMBL;AL078579; GSPDB:GN00062; ATSP:T27E11.70
A;Experimental source: cultivar Columbia; BAC clone T27E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 517
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Pred. No. 42;
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A;Cross-references: EMBL:AF035384; PIDN:AAC39467.1
A;Experimental source: cultivar ecotype Col-O; leaf
C;Genetics:
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A,Note: induced during leaf senescence
C,Superfamily: endoxyloglucan transferase
C,Keywords: phosphotransferase; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.4%;
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63.6%;
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Matches 6; Conservative
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Matches 7; Conservative
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A; Molecule type: DNA
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Isoid=P81278-2; Sequence=VSP_004370;
-!-TISSUB SPRCIFICITY: Widely expressed, with highest levels in medula oblongata and hypothalamus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley; TISSUE-Hypothalamus;
Anderson S.T., Kokay I.C., Lang T., Grattan D.R., Curlewis J.D.;
"Quantitation of prolactin-releasing peptide (PrRP) mRNA expression in
specific brain regions during the rat oestrous cycle and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor.";
Regul. Papt. 83:1-10(1999).
-!- PUNCTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate accoracin of prolactin through its receptor GPR10. May stimulate accoracin propriety to secrete PRL.
-!- ALTERNATIVE PRODUCTS:
-!- ALTERNATIVE PRODUCTS:
- Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hindma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S., Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M., Kurokawa T., Nishimura O., Onda H., Fujino M.;
M. prolactin-releasing peptide in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99426652; PubMed=10498338; Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S., Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H., Sumino Y., Fujino M.; Tissue distribution of prolactin-releasing peptide (PrRP) and its
                                                                                                                                                                                                                                                                                                                                                                        P81278, 08K3Y0;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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MEDLINE=98268781; PubMed=9607765;
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IISSUE SPECIFICITY.
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DGRTKFSQRG -> SECLTYGKQPLTSFHPFTSQMPP (in
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"A prolactin-releasing peptide in the brain.",

Nature 393:272-276(1998).

-!-FUNGTION: Stimulates prolactin (PRL) release and regulates the expression of prolactin through its receptor GPR10. May stimulate lactorrophs directly: Medulla oblongata and hypothalamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2003 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) (Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION (G-53 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
PROLACTIN-RELEASING PEPTIDE PRRP31.
PROLACTIN-RELEASING PEPTIDE PRRP20.
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PROLACTIN-RELEASING PEPTIDE PRRP20.
                                                                                                                                                    EMBL, AB015418; BAA29026.1; -.
EMBL, AF521930; AAM82154.1; -.
PIR, JC7607; JC7607; JC7607; Amidation; Signal; Cleavage on pair of basic residues;
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Hormone, Amidation; Signal; Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 79; DB 1; Length 83; Pred. No. 2.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOC75A264EEE4F29 CRC64;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                     Alternetive splicing. 21 SIGNAL 22 SIGNAL 22 PEPTIDE 33 S2 PROPEP 57 83 MOD RES 52 VARSPLIC 33 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
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P81264;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99426652; PubMed=10498318;
Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,
Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sumino Y., Fujino M.; "Tissue distribution of prolactin-releasing peptide (PrRP) and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2010 (Rel. 41, Last annotation update)
Prolactin-releasing peptide precursor (PrRP) (Prolactin-releasing hormone) [Contains: Prolactin-releasing peptide PrRP31; Prolactin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                        AMIDATION (G-54 PROVIDE AMIDE GROUP) 08AC35A13B0FA908 CRC64;
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PROLACTIN-RELEASING PEPTIDE PRRP20.
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                                                                                                         Score 74; DB 1; Length 98;
Pred. No. 1.9e-05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        87 AA.
                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=98268781; PubMed=9607765;
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98
53
10544 MW;
                                                                                                         th 93.7%;
1 Similarity 92.3%;
12; Conservative
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84.6%;
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                                                                                                                                                                                                                              1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                 TPDINPAWYAGRG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               releasing peptide PrRP20]
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                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                  Query Match
Best Local Similarity
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REPUBLINE FROW N.A.

RAP SEDUBLINE FROW N.A.

RA BARGUENCE FROW N.A.

RA BARGUENCE TO Andre B. Arnold W., Bahr A., Ballesta J.P.G.

RA BARGUENCE TO BECKER A., Bliteau N., Blocker H., Blugeon C.,

RA BOSKOVIC J. Brandt P., Bruckerner M., Buitrago M.J., Coster F.,

RA BOSKOVIC J., Backer B., Granotier C., Hanemann V., Hankeln T.,

RA Gomez-Feris A., Granotier C., Hanemann V., Hankeln T.,

RA Hoheisel J.D., Jaeger W., Jimenz A., Jonniaux J.-L., Kraemer C.,

RA Monnet A., Moro M., Mueller Auer S., Nussbauwer B., Paricio N.,

RA Prydz H., Purnelle B., Rasmussen S.W., Remacha M., Rewelta J.L.,

RA Prydz H., Purnelle B., Rasmussen S.W., Remacha M., Rewelta J.L.,

RA Scharfe M., Salom D., Saluz H.P., Saiz J.E., Saren A.-M., Schaefer M.,

RA Scharfe M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,

RA Wagner G., Wamburt R., Wedler E., Wedler H., Woelf S., Harris D.E.,

RA Bowman S., Brown D., Churcher C.M., Connor R., Dedman K., Gentles S.,

RA Hamlin N., Hunt S., Jones L., McDonald S., Murphy L., Niblett D.,

RA Arujo R., Aviles E., Berno A., Garpenter J., Cherry J.M.,

RA Lashkari D., Lew H., Lin D., Mosedale D., Schramm S., Schroeder M.,

RA Lashkari D., Lew H., Lin D., Mosedale D., Schram S., Coherry J.M.,

RA Chung E., Duncan M., Hunicke-Smith S., Hamman R., Cooper J., Ding H.,

RA Davis R.W., Johnston M., Andrews S., Brinkman R., Googer J., Hallier L.W., Jier M., Volnscon L., Wallem P.,

RA Hawkins J., Hillier L.W., Jier M., Volnscon D., Rikkin L.,

RA Hawkins J., Hillier L.W., Jier M., Johnson D., Johnston L., Malles D., Wilchen D., Wilchen C., Wilchen R., Marerston R., Albermann K., Hani J., Heumann R., Hanton M., Wilson R., Walerskin B., Wilcher R., Meerston R., Albermann K., Han H., Lin R., Mercharland P., Racheriala P., Hander R., Paller R., Racher B., Wilcher R., Meerston R., Albermann R., Racher R., Willer R., Waler R., Albermann R., Racher R., Willer R., Waler R., Racher R., Rach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The nucleotide sequence of Saccharomyces cerevisiae chromosome IV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=X2180;
MEDLINE=93330299; PubMed=8336735;
Bauer F., Urdaci M., Aigle M., Crouzet M.;
"Alteration of a May protein leads to conditional viability with defects in cytoskeletal and budding patterns.";
Mol. Cell. Biol. 13:5070-5084(1993).
                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomyoota; Saccharomyootina; Saccharomyoetes; Saccharomyoetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
                                                                                                                                                                                     01-FBB-1995 (Rel. 31, Created)
01-FBB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Reduced viability upon starvation protein 167-
RS167 OR YDR388W OR D9509.8.
Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                              482 AA
                                                                                                                                              PRT;
1 TPDINPAWYTGRG 13
                                    34 TPDINPAWYASRG 46
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 387:75-78(1997).
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30-MAY-2000 (Rel. 39, Last sequence update)
15-MAX-2004 (Rel. 43, Last annotation update)
GRB2-related adaptor protein 2 (GADS protein) (Growth factor receptor binding protein) (GRB1G) (GRB-2-like protein) (GRB2L) (Hematopoietic cell-associated adaptor protein) GRB-2-like protein) (GRB-2-like protein) (GRB-2-monocytic adapter) protein) (Monocytic adapter) (MONA) (Adapter protein GRID).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.3%; Score 44.5; DB 1; Length 482; 66.7%; Pred. No. 6.9;
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Binds to actin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 AA
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                                                   -!- SIMILARITY: Contains 1 BAR domain.
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Kedra D., Dumanski J.P.;
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Best Local Similarity
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SEQUENCE FROM N.A.
Kedra D., Dumanski J.P.;
"Cloning of the human and mouse growth factor receptor binding protein
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075791; 043726;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
binding protein) (GRBLG) (Grf40 adaptor protein) (Grewth factor receptor binding protein) (GRB2) (GRB40 adaptor protein) (GRB2) (RRB-2-like protein) (GRB2) (RRB) (HRB (CRB2) (GRB2) (RRB) (HRB (CRB2) (GRB2) (RRB) (R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=99097254; PubMed=9878555;
Qiu M., Aua S., Agrawal M., Li G., Cai J., Chan E., Zhou H., Luo Y.,
Liu M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human),
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Teramoto T., Nagashima M., Terai S., Thorgeirsson S.S.;
"GrbX, new recruited signaling gene having homology with Grb2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.4%; Score 43; DB 1; Length 322; 75.0%; Pred. No. 8.2; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           736311D0640CD3D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 2.
PROSITE; PS50001; SH2; 1.
SH2 domain; SH3 domain; Repeat.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3 2.
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36810 MW;
                                                 InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 2.
PRINTS; PR00401; SH3DOMAIN.
PRODOM; PP000093; SH3DOMAIN.
ProDOM; PD000096; SH3; 2.
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Best Local Similarity 75.0%,
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322 AA;
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SEQUENCE FROM N.A.
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TISSUE=Blood;
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ID GRP2_HUMAN

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DT 30-MAY.

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REDLINE-22388257; PubMed-12477932;

REDLINE-22388257; PubMed-12477932;

REDLINE-22388257; PubMed-12477932;

RETAINSEQUER. Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.

RA Diacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.

RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

RA Brans S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., Wackernan K.J., Malek J.A., Gunarane P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Bakesley R.W., Touchman J.W., Scheurtz J., Myers R.M.,

R Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R Budes S.J. Worl S.J., US.A., 99:1689-16903(2002).

- FUNCTION: Interacts with SLP-76 to regulate NF-AT activation.

E Binds to tyrosine-phosphorylated shc.

- SIMILARITY: Contains 2 SH3 domain.

C - SIMILARITY: Contains 2 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ellis J.H., Ashman C., Burden M., Kilpatrick K.E., Morse M.A., Hamblin P.A., "GRID, a novel Grb2-related adapter protein which interacts with the activated T cell co-stimulatory receptor CD28."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99087328; PubMed=9872323;
Liu S.K., McGlade C.J.;
Gads is a novel SH2 and SH3 domain-containing adaptor protein that binds to tyrosine-phosphorylated Shc.";
Oncogene 17:3073-3082(1998).
                                        Bourette R.P., Arnaud S., Myles G.M., Rohrschneider L.R.,
Blanchet J.P., Mouchiroud G.,
"Mona, a novel hematopoietic-specific adaptor interacting with the
macrophage-colony-stimulating factor receptor, is implicated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ů
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                                                                                                                                                                                                                  monocyte/macrophage development.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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BMBL, AF055465; AAD08803.1; -.
EMBL, AF053405; AAD40869.1; -.
EMBL, AF129477; AAD41783.1; -.
EMBL, AF236118; AAF60318.1; -.
EMBL, BC052496; AAH52496.1; -.
HSSP; P29354; 1GR1.
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SEQUENCE FROM N.A
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Tanaka N.,

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RY STAIN-cv. Columbia,

RY AND STAIN-cv. Columbia,

RY MUDINE-2003488; PubMed=10617198;

RY MUDINE-2003488; PubMed=10617198;

RY AND STAIN-cv. Stiekema W., Entian K.-D., Terryn N.,

RA Mayer K.F.X. Schneller C., Wandt W., Entian K.-D., Terryn N.,

RA Haris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Mueller M.,

RA Keicher B., Portectale D., Perez-Alonso M., Schmidtheini T.,

RA Hoheisel J., Zimmermann W. Wedler H., Ridley P.,

RA Langham S.-A., McCullagh B., Bilham L., Robben J.,

RA Langham S.-A., McCullagh B., Bilham L., Robben J.,

RA Meizenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

RA Meizenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

RA Mooijman P., Klein Lankhorst R., Rose W., Hauf J., Koetter P.,

RA Mooijman P., Klein Lankhorst R., Wan Staverem M., Dirkse W.,

RA Mooijman P., Klein Lankhorst R., Van Staverem M., Noclay K.,

RA Mooijman P., Rajandream M.A., Lyne M., Lennard N., McLay K.,

RA Montagu M., Rogers J., Cronin A., Quail M.A., Brav-Allen S.,

RA Pettett A., Rajandream M.A., Lyne M., Lennard N., Mueller-Auer S.,

RA Borkova D., Bloecker H., Scharfe M., Grimm M., Lochnert T.-H.,

RA Borkova D., Bloecker H., Scharfe M., Grimm M., Lochnert T.-H.,

RA Borkova D., Bloecker H., Scharfe M., Grimm M., Lennard S., Herzl A.,

RA Borkova D., Bloecker H., Scharfe M., Grimm M., Lennard S., Herzl A.,

RA Borkova D., Bloecker H., Scharfe M., Grimm M., Rogers S.,

RA Massenet O., Quigley F., Clabauld G., Muendlein A., Pelber R.,

Robenst S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
                                                                                                                                                                                                                                                                                                                                                             D XX24 ARATH STANDARD; PRT; 269 AA.

C P24806; O64956; O39148; Q39149; Q41904; Q8LDQ0;

T O1-MAR.1992 (Rel. 21, Created)

T 28-FEB-2003 (Rel. 41, Last sequence update)

Y SPAR-2004 (Rel. 43, Last annotation update)

Xyloglucan endotransglucosylase/hydrolase protein 24 precursor

EC 2.4.1.207) (At-XTH24) (XTH-24) (Meristem protein 5) (MERI-5

Protein) (MERIS protein) (Endo-xyloglucan transferase) (Xyloglucan ando-1,4-beta-D-glucanase)

XTH24 OR MERI-5 OR MERISB OR SEN4 OR AT4G30270 OR F9N11.120.

A rabidopsis thaliana (Mouse-ar cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; curosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medford J.I., Elmer J.S., Klee H.J.; "Molecular cloning and characterization of genes expressed in shoot
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0
                                                                                                                                            54.4%; Score 43; DB 1; Length 330; 75.0%; Pred. No. 8.4; tive 2; Mismatches 0; Indels
                                                                                                                                                                                       0; Indels
                     SH2.
SH3 2.
L -> F (in dbSNP:12759).
/FTIG=VAR 012079.
W; 74F4C8D0EBB56D55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Kamimai T., Tomita E., Nishitani K.;
Submitted (UUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
    SH3 1.
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                                                                                                   330 AA; 37909 MW;
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                                                                                                                                                                                     Conservative
                                                                                                                      Query Match
Best Local Similarity (
                                                                                                                                                                                                                                                 305 NPSWWTGR 312
                                                                                                                                                                                                                         5 NPAWYTGR 12
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RA Cheedor F. Nobel R., Barger C., Monfort A., Casacuberta E., Torsea A., Casacuberta E., Raber R., Barger C., Monfort A., Casacuberta E., A., Casacuberta E., Raber E., Purine I., Schwarz S., Schollar E., Enghese T., Facher C., Raber B., Maria E., Barder E., France C., Raber B., Maria C., Schwarz S., Schollar E., Enghes E., France C., Paramel I., Debdia N., Wilson R.K., de la Bastide M., Marzey G., Shares D., Casaca T., Rhenna C., Schoka C., Shares E., Schoka C., Schollar E., Rhenna C., Shares E., Schoka C., Shares E., Marchi E., Shares E., Schoka C., Shares E., Marchi E., Shares E., Schoka C., Shares E., Cortea M., Abu-Threiden J., Mink P. Bentle C., Shares E., Shares E., Shares E., Shares E., Cortea M., Abu-Threiden J., Mink P. Bentle C., Shares E., Doore K., Cotton M., Joshu C., Rhenna D., Spieth J., Eyna E., Adrese S., Gaisel C., Layman D., Rhenson G., Shares M., Strong C., Shares M., Lama C., Shares E., Marzer M., Marcia E., Danes K., Pepil K., Cotton M., Joshu C., Rhenna C., Shares E., Shokay M., Hasesgas A., Hansed A., Lodhi M., Johnson A., Raby I. K., Shares M., Marcia E., Shokay M., Hasesgas A., Hansed M., Lodhi M., Johnson A., Raby J., K., Shares M., Marcia E., Shokay M., Marcia E., Shares M., Marcia M., Sakan H., Shares G., Shokay M., Hasesgas A., Hansed M., Lodhi M., Johnson A., Raby J., K., Marcia M., Shares M., Marcia M., Sakan H., Wu T., Yu G., Karane W., Sagumer G., Shares M., Marcia M., Sakan H., Shares G., Link G., Canadde G., Lodhi M., Wa H.C., Shares M., Marcia M., Sakan H., Wu T., Yu G., Karane M., Sagumer G., Marcia M., Marci
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DB 1; Length 269;

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Plant J. 18:371-382(1999)
                 Arabidopsis.";
                             NOMENCLATURE
        Arabidopsis.
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53.2%;
Query Match
Best Local Similarity 63.5-
Best Ar Conservative
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es 6; Conserv
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ID YAAJ_ECO
AC P30143;
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Rose J.K.C., Braam J., Fry S.C., Nishitani K.;
Rose J.K.C., Realyzes xyloglucan endohydrolysis (XEH) and contransglycosylation (XET). Cleaves and religates xyloglucan endohydrolysis (XEH) and chereby participates in cell wall construction of growing tissues.

May be required during development to modify the walls of cells under mechanical stress.

C. CAPALYTIC ACTIVITY: Breaks a beta-(1->4) bond in the backbone of a xyloglucan and transfers the xyloglucanyl segment on to O-4 of the conn-reducing terminal glucose residue of xyloglucan or an oligoseccharide of xyloglucan.

C. CAPALYTIC ACTIVITY: Brooks a beta-(1->4) bond in the backbone of a xyloglucan or an oligoseccharide of xyloglucan.

C. SUBCELILLAR LOCATION: Apoplast (Probable).

C. SUBCITION: May be transcriptionally regulated by ANGUSTIFOLIA.

C. PPM: Contains at least one intrachani disulfide bond essential for its enzymatic activity.

C. PPM: N-glycosylated, essential for its enzymatic activity.

C. PPM: N-glycosylated, essential for its enzymatic activity.

C. SUBCELILLON: Ref. Sequence differs from that shown due to frameshifts in positions 158; 178; 183; 189; 190; 194 and 199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21886176; PubMed=11889033; Kim G.-T., Shoda K., Tsuge T., Cho K.-H., Uchimiya H., Yokoyama R., Nishitani K., Tsukaya H.;
"The ANGUSTIPCLIA gene of Arabidopsis, a plant CtBP gene, regulates leaf-cell expansion, the arrangement of cortical microtubules in leaf-cells and expression of a gene involved in cell-wall formation.";

EMBO J. 21:1267-1279(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21530286; PubMed=11673616;
MEDLINE=21530286; PubMed=11673616;
Yokoyama R., Mishitani K.;
"A comprehensive expression analysis of all members of a gene family encomprehensive expression analysis of all members of a gene family regions involved in cell-wall construction in specific organs of
                                                                                                                                                                                                                                                                ENZYMATIC ACTIVITY, AND N-GLYCOSYLATION.
MEDLINE=99334624; PubMed=10406121;
Cambbell P., Bream J.;
"In vitro activities of four xyloglucan endotransglycosylases from
                                                   Arrowsmith D.A., De Silva J., "Characterisation of two tomato fruit-expressed cDNAs encoding "Characterisation of two tomato"; "xyloglucan endo-transglycosylase."; plant Mol. Biol. 28:391-403(1995).
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DATABASE: NAME=XTH-World;
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a phage system for mycobacterial genetics.";
Mol. Microbiol. 7:395-405(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
L5-like viruses.
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85.7%; Pred. No. 5.4;
tive 1; Mismatches (
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01-UUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Gene 30 protein (GP30)
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Score 42; DB Pred. No. 10; 1; Mismatches
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MEDLINE=93211282; PubMed=8459766;
Hatfull G.F., Sarkis G.J.;
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC transpo
InterPro; IPR004602; Uvrā.
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259 2
359 3
569 AA;
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                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are extrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                           "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                              STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plubkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UVRABC System protein A (UvrA protein) (Excinuclease ABC subunit A)
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EMBL, AB000111; AAC73118.1; -.

ENGGENE, EG11555; YaaJ.

InterPro; IPR001463; NaA/rel_permeasel.

InterPro; IPR001463; NaA/Ala_symport.

Pfam; PF0125; Na Ala_symp; 1.

PRINTS; PR00175; NaALASMPORT.

ITGRPAM; ITGRO0835; agcs; 1.

PROSITE; PS00873; Na ALANINE SYMP; 1.

Hypothetical protein; Transmembrane; Iransport;
                                                                                                                                                                      [Potential].
-1- SIMILARITY: BELONGS TO THE SODIUM:ALANINE SYMPORTER FAMILY (SAF). STRONG, TO H.INFLUENZAE HI0183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vitreoscilla stercoraria.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Vitreoscilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 1; Length 476; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2F6EB2E12E126E63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  569 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Symport; Complete proteome.
TRANSMEM 4 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
[2]
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
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TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
UVRA VITST
ID UVRA V.
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[1] SEQUENCE FROM N.A. NCBI_TaxID=61;

Matches

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STRAIN=C1;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            lesions (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.
Liu S.C., Liu Y.X., Webster D.A., Stark B.C.;
Sequence of the region downstream of the Vitreoscilla hemoglobin gene: vgb is not part of a multigene operon.";
Appl. Microbiol. Biotechnol. 42:304-308(1994).
-!- FUNCTION: The UVTABC repair system catalyzes the recognition and processing of DNA lesions. UVTA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvTA and 2 uvTB subunits scans DNA for abnormalities. When the presence of a lesion has been verified by uvTB, the uvTA molecules dissociate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promis PRO0005; ABC transporter; 1.
Probom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; I.
TIGRRAMS; TIGR00630; uvra; 1.
PROSITE; PS00211; ABC TRANSPORTER_1; 2.
PROSITE; PS00893; ABC TRANSPORTER_2; 2.
SOS response; Excision nuclease; DNA repair; DNA recombination;
DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                        (By similarity). SUBUNIT: Forms a heterotetramer with uvrB during the search for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAINA-RACT 31821, ZM4 / CP4;

Kang H.L., Jin S.J., Kang H.S.;

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-!- PUNCTION: The UvrABC repair system catalyzes the recognition an processing of DNA lesions. UvrA is an ATPase and a DNA-binding processing of DNA lesions. UvrA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvrA and 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
UVZBC system protein A (UvrA protein) (Excinuclease ABC subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zymomonas mobilis.
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Zymomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          687 TPRSNPATYTG 697
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es 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=83334;
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Q8X5U9;
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                                                                                                                                                                                PIR, 733732; T33732.
HAWAP; MF 00205; atypical; 1.
InterPro; IPR003439; ABC transporter.
Pfam; PF0000005; ABC transporter; 1.
Probom; P0000005; ABC transporter; 1.
PROSTIE; P500211; ABC TRANSPORTER 1; 2.
PROSTIE; P500211; ABC TRANSPORTER 1; 2.
PROSTIE; P50011; ABC TRANSPORTER 1; 2.
PROSTIE; P50011; ABC TRANSPORTER 1; 2.
PROSTIE; P50011; ABC TRANSPORTER 1; 2.
DNA excision; ATP-binding; DNA repair; DNA recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97394467; PubMed=9252185;

MEDLINE=97394467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.E., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FirzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weldman J.M., Fujil C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: The UvrABC repair system catalyzes the recognition and
uvrB subunits scans DNA for abnormalities. When the presence of lesion has been verified by uvrB, the uvrA molecules dissociate
                    (By similarity). SUBUNIT: Forms a heterotetramer with uvrB during the search for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
UVIRBC system protein A (UvrA protein) (Excinuclease ABC subunit A)
UVRA OR HP0705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                         51.9%; Score 41; DB 1; Length 925; 72.7%; Pred. No. 51; 3; Indels iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                   101648 MW; 8AF0C36C83712AC5 CRC64;
                                                                                                                                                                                                                                                                                                                     ATP (POTENTIAL)
ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                         EMBL; AF086791; AAC70369.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          TPRSNPATYTG 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 388:539-547(1997)
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651
769
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925 AA;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                           Zinc-finger.
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P56474;
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NP_BIND
ZN_FING
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UVRA_HELPY
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processing of DNA landers, United and Annual An
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8; Conservative
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640
740
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940 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.cib.ch).
                                                                                                                                                                                            Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Ind T., Takami H., Hattori M., Shinagawa H., Ruhara S., Shiba T., Hattori M., Shinagawa H.; Ruhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Escherichia coli Complete genome sequence of enterohemorrhagic Escherichia coli DIS.H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).

-!- FUNCTION: The UvrAbC repair system catalyzes the recognition and processing of DNA lesions. UvrA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of a lesion has been verified by uvrB, the uvrA molecules dissociate (By similarity).

-!- SUBUNIT: Forma a heterotetramer with uvrB during the search for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAWAP; MF 00205; -; 1.
InterPro; IPR001439; ABC transporter.
InterPro; IPR00465; Uvrā.
InterPro; IPR004605; Uvrā.
ProDom; PD000006; ABC transporter; 1.
ProDom; PD00001; ABC transporter; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 2.
PROSITE; PS00313; ABC TRANSPORTER 2; 1.
SOS response; Excision nuclease; DNA repair; DNA recombination; DNA excision; ATP-binding; Repeat; Zinc; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-0CT-2003 (Rel. 42, Last sequence update)
10-6CT-2003 (Rel. 42, Last annotation update)
UVRABC system protein A (UVRA protein) (Excinuclease ABC subunit A)
UVRA OR C5048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Pred. No. 51;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280 C4-TYPE.
447 ATP (POTENTIAL).
66 C4-TYPE.
103884 MW; A20C90C935A0ACEB CRC64;
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                                                                                                                 STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacteriaceae, Escherichia.
NCBI_TaxID=217992;
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NP_BIND 31 38 AT
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10-OCT-2003 (Rel. 42, Last seq
10-OCT-2003 (Rel. 42, Last ann
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72.7%;
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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08FB02;
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SEQUENCE
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UVRA_ECOL6
UVRA_ECOL6
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (By similarity).
SUBUNIT: Forms a heterotetramer with uvrB during the search for lesions (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.
STRAIN=06:HI / CFT073 / ATCC 700928;
MEDLINE=2898244; Pubmed=12471157;
MEDLINE=2898244; Pubmed=12471157;
Melch R., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              đ
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InterPro; 1PR003493 ABC transporter.
InterPro; 1PR004602; UvEA.
Pfam; PF000065; ABC tran; 1.
Pr000m; PD000066; ABC transporter; 1.
TIGREAMS; TIGR00630; uvEA; 1.
PROSITE; PS00211; ABC TRANSPORTER_1; 2.
PROSITE; PS0993; ABC TRANSPORTER_1; 2.
PROSITE; PS0993; ABC TRANSPORTER_2; DNA recombination;
DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
                                                                                                                                                                                                                                                   of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
Processing of DNA lesions. UvrA is an ATPase and a DNA-binding protesin. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of lesion has been verified by uvrB, the uvrA molecules dissociate
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UVYABC system protein A (UVYA protein) (Excinuclease ABC subunit A).
UNFAR OR DINE OR B4058 OR SF4146 OR S3583.
Shiqella flever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Pred. No. 51;
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647 ATP (POTENTIAL).
776 C4-TYPE.
103882 MW; A20C90C93816ACEB CRC64;
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NCBI_TaxID=562, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger; Complete proteome.
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uvrB subunits scans DNA for abnormalities. When the presence of lesion has been verified by uvrB, the uvrA molecules dissociate

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Search completed: August 12, 2004, 14:44:53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=2272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Ehen Y., Lu W., Wang J., Liu H.,
Jin O., Yuang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89380205, PubMed=2550431, Navaratnam 5., Myles G.M., Strange R.W., Sancar A.; Navaratnam 5., Myles G.M., Strange R.W., Sancar A.; Evidence from extended X-ray absorption fine structure and site-specific mutagenesis for zinc fingers in UvrA protein of Escherichia
                                                                                                                                                                                                                  "Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes.";
Nucleic Acids Res. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                            SPECIESEE.coli,
MEDLINE=83299251; PubMed=6310514;
Backendorf C., Barndsma J.A., Kartasova T., van de Putte P.;
In vivo regulation of the uvrA gene: role of the '-10' and '-35'
promoter regions.";
Nucleic Acids Res. 11:5795-5810(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SPECIES=S.flexneri, STRAIN=2457T / ATCC 700930 / Serotype 2a;

SPECIES=S.flexneri, STRAIN=2457T / ATCC 700930 / Serotype 2a;

MBDLINE=2559074, Pubmed=12704152;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Fournier G., Mayhew G.F., Plunkett G. III, Rose D.G., Darling A.,

Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blattner F.R.;

"Complete genome sequence and comparative genomics of Shigella

flexneri serotype 2a strain 2457T.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=82220077; PubMed=6283374; Sancar A., Sancar G.B., Rupp W.D., Little J.W., Mount D.W.; Flex& protein inhibits transcription of the E. coli uvrA gene in vitro."; Nature 298:96-98(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=E.coli;
MEDLINE=91208117; PubMed=1826851;
MYles G.M., Sancar A.;
"Isolation and characterization of functional domains of UvrA.";
Biochemistry 30:3834-3840(1991).
           MEDLINE=86168204; PubMed=3007478;
Husain I., van Houten B., Thomas D.C., Sancar A.;
"Sequences of Escherichia coli uvrA gene and protein reveal two
pocential ATP binding sites.";
J. Biol. Chem. 261:4895-4901(1986).
                                                                                                                       SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=94089392; PubMed=8265357;
Blatter F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
Daniels D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-14 FROM N.A.
                                                                                                                                                                                                                                                                            [3]
SEQUENCE OF 1-25 FROM N.A.
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SPECIES=E.coli;
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coli.",
J. Biol. Chem. 264:16067-16071(1989).

-!- FUNCTION: The UvrABC repair system catalyzes the recognition and
processing of DNA lesions. UvrA is an ATPase and a DNA-binding
protein. A damage recognition complex composed of 2 uvrA and 2

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REML; W00006; AAC4152.1; ---

REML; X01621; CAA25764.1; ---

REML; X01621; CAA25764.1; ---

REML; X01721; AAA24753.1; ---

REML; ABC16423; AAA6568.1; ---

REML; ABC16429; AAA6568.1; ---

REML; ABC16429; AAA6568.1; ---

REML; ABC16429; AAA6568.1; ---

REML; ABC1643; AAA6568.1; ---

RECO2DBA55; H124.0; FTH EDITION.

RECOGENE; EG11061; UVTA.

RECOGENE; EG11061; UVTA.

RECOGENE; PRO004602; UVTA.

RECOGENE; PRO00066; ABC_transporter.

RECOGENE; PRO00066; ABC_transporter.

RECOGENE; PRO00066; ABC_transporter.

RECOGENE; PRO0011; ABC_TRANSPORTER_1; 2.

RECOGENE; PROS011; ABC_TRANSPORTER_2; 1.

RECOGENE; PROS011; AAA6, TRANSPORTER_2; 1.

RECOGENE; PROS011; AAA6, TRANSPOR
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253 280 C4-TYPE.
640 647 ATP.
740 766 C4-TYPE.
253 253 C->A,H,S: REDUCED ACTIVITY.
940 AA; 103867 MW; D61AAEB6514B860C CRC64;
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C4-TYPE.
ATP.
C4-TYPE.
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NP.BIND 31 38
ZM_FING 253 280 C4-
ZM_FING 740 647 ATP
ZM_FING 740 766 C4-
MUTAGEN 253 253 C->
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les 8; Conservative
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Sequence:

on:

Searched:

Database

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Q8r054 mus musculu Q8k1fs mus musculu Q91fa0 arabidopsis Q8tts7 methanosarc Q7u4h3 synechococc Q7u4h3 synechococc Q8x27 c chloropla Q39562 chlamydomon Q8bfe9 uncultured Q9brb7 homo sapien Q27142 methanobact Q9134 arabidopsis Q8613 pseudomonas Q91x8 homo sapien Q82x2 pyrobaculum Q82x2 pyrobaculum Q2xv2 pordetella Q7w15 bordetella Q7w15 bordetella Q7w11 bordetella Q88b54 pseudomonas Q88rg2 pseudomonas
  001498 caenorhabdi
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Preproprolactin-releasing peptide.
Ovis aries (Sheep).
Darazyota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 98 AA; 10513 MW; 2A53331ED62CAABS CRC64;
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Last annotation update)
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001498
Q8R1F8
Q8R1F8
Q9LFA0
Q8TTS7
Q7U4H3
Q8WKZ7
Q39562
Q8BFE9
Q9BFE9
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0951P4
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Copyright (c) 1993 - 2004 Compugen Ltd.
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7; Conservative
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                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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Pred. No. 0.24;
3; Mismatches 2; Indels
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Pred. No. 1;
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                                                                                                                                                                                                                              TISSUE=Brain;
Satake H., Minakata H., Fujimoto M.;
"Carassius RFamide (C-RF amide).";
"Carassius RFamide (C-RF mide).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020024; BAA76662.1; -
SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lawlor S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035608; CAB55682.1;
NON TER 54 54 ....
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Sushi-repeat protein (Sushi-repeat containing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
DJ479J7.3 (Sushi-repeat protein (SRPUL)) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 AA.
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01-AUG-1998 (TrEMBLrel. 07, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                           Carassius auratus (Goldfish).
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53.8%;
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SEQUENCE FROM N.A.

A Huang C.-H., Chen H., Peng J., Chen Y.;

"Cloning and characterization of the sushi-repeat containing protein
"Cloning and characterization of the sushi-repeat containing protein
"Cloning and characterization partner of Rh type C glycoprotein
"Grap) as a noch interaction partner of Rh type C glycoprotein
"T (SRP) as a noch interaction partner of Rh type C glycoprotein
"I submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

BRBL, AF393649; AAG15765.1; -.

R EMBL, AF393649; AAG15765.1; -.

R DATA: AAG15763.1; -.

R DATE: PRO004118; P:electron transport; IEA.

R InterPro; IPR000128; Cytochrome_P450.

R InterPro; IPR000436; Sushi_SCR_CCP.

Pfan; PF000494; HYR; 1.

R InterPro; IPR00044; Sushi_SCR_CCP.

Pfan; PF000496; CytoCHROME P450; 1.

R PROSITE; SO0066; CYTOCHROME P450; 1.
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
L Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
R GO, GO:0006118; P:electron transport; IEA.
R InterPro; IPR003410; Hyalin.
R InterPro; IPR003410; Hyalin.
R InterPro; IPR003410; Hyalin.
R InterPro; IPR003410; Hyalin.
R Ffam; PF02494; HYR; 1.
R Ffam; PF00084; sushi, 3.
R MART; SMART; SMO032, CCP; 3.
R PROSITE; PS00086; CYTOCHROME P450; 1.
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Pred, No. 10;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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Pred. No. 10;
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PRELIMINARY;
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     SEQUENCE
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Q20170;
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Q9Y276;
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                                                            MEDLINE=20504483; PubMed=11016950; Mg W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shrogna S.P., Mahairas G.G., Derquist B., Pan M., Shrogna J., Shukla H.D., Lasky S.R., Baliga N.S., Thorson V., Sbrogna J., Swartzell S., Weit D., Hall T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S., Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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61.5%; Pred. No. 8.7;
ative 1; Mismatches 4; Indels
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"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"More A Roof 928-2001) to the EMBL/GenBank/DDBJ databases.
BMB.; AF06 93175; T33175.
"NormPep: C24G.6; CE17462.
"WormPep: C24G.6; CE17462.
"MormPep: C24G.6; Pelectron transport; IEA.
InterPro; IPR002937; Amino oxidase.
InterPro; IPR002055; NAD BS.
Pfam; PF01593; Amino_oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
Greco T., Bradshaw H., Keppler D.;
"The sequence of C. elegans cosmid C24G6.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
Archaea, Buryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                               139 AA; 15463 MW; 691F4E01A191F8CE CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             527 AA.
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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InterPro; IPR005175; DUF296.
Pfam; PF03479; DUF296; 1.
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les 8; Conservative
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SEQUENCE 139 AA;
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Matches
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"Identification and characterization of human cDNAs specific to BCS1, PET112, SCO1, COX15, and COX11, five genes involved in the formation and function of the mitochondrial respiratory chain.";
[2]
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
C. elegans WRT-3 protein (Corresponding sequence F38E11.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
                                                     Length 527;
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z68342; CAA92775.2;
SEQUENCE 179 AA; 20965 MW; F9FA6891A2BF2BDD CRC64;
527 AA; 59805 MW; 9FBB1FB84437C5CB CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
HOSCI (BCSI (Yeast homolog)-like).
BCSI OR BCSIL.
Homo sapiens (Human).
                                                  58.2%; Score 46; DB 5; 58.3%; Pred. No. 36; ative 2; Mismatches
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MEDLINE=99097350; Pubmed=9878253;
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                                                     Query Match 58.2
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                          370 PNVLSAWYAGRG 381
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Matches 6; Conservative
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211 NPKWYTDRG 219
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sapiens (Human).
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Best Local Similarity
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NCBI TaxID=7955;
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                                                                                                                              NCBI_TaxID=9606;
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Q7ZV60
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Sucmalainen A., Peltonen L.;

"GRACILE syndrome, a lethal metabolic disorder with iron overload, is caused by a point mutation in BC31L.";

Am. J. Hum. Genet. 71:863-876 (2002).

BMBL; AF026849; AAD08658.1; -.

BMBL; AF0368195; AAR09417.1; -.

BMBL; AF038195; AAR09417.1; -.

BMBL; BC000146; AAH00416.1; -.

BMBL; BC000146; AAH00416.1; -.

BMBL; BC0005700; AAH00416.1; -.

Genew, HGNC1.020; BCS1L; -.

GO GO:0005750; Crespiratory chain complex III (sensu Bukarya); TAS.

GO; GO:0005790; Crespiratory chain complex III (sensu Bukarya); TAS.

GO; GO:0005790; Crespiratory chain complex III (sensu Bukarya); TAS.

GO; GO:0005790; Crespiratory chain complex assembly; TAS.

HITCEPTO; IPR003999; AAA ATPasse.centr.

Pfam; PR001004; AAA; 1.

SMART; SM00382; AAA; 1.

SMART; SM00382; AAA; 1.

SWART; SM00382; AAA; 1.
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"Mutations in bcs1, a mitochondrial respiratory chain assembly gene, are responsible for the complex III deficiency of patients with tubulopathy and liver failure."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22233229; PubMed=12215968;
Visapaa I., Fellman V., Vesa J., Dasvarma A., Hutton J.L., Kumar V.
Payne G.S., Makarow M., Van Coster R., Taylor R.W., Turnbull D.M.,
                                                                                                                                  Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.; "A 'double adaptor' method for improved shotgun library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
"Large-scale concletenation cDNA sequencing.";
Genome Res. 7:353-358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686K10234.
                                                                                              MEDLINE=96207227; PubMed=8619474;
                                                                                                                                                                                                                                                                Anal. Biochem. 236:107-113(1996)
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 NPKWYTDRG 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                            construction.";
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Q722V7;
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DT AC OCT
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio regio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii; Teleostei, Ostariophysi, Cypriniformes;
                                                                                                                                                   Weil
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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                                                                                                 57.0%; Score 45; DB 13; Length 420;
llarity 77.8%; Pred. No. 41;
Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                        Score 45; DB 4; Length 419;
Pred. No. 41;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE_DOCA;
Straubberg N.;
Straubberg N.;
Straubberg N.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC45990; AAA145990.1; -..
GO; GO:0000166; F:ATP binding; IEA.
GO; GO:0000166; F:ATP binding; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003599; AAA_ATPase.
Ffam; PF00004; AAA; 1.
SMAAT; SM00382; AAA; 1.
SEQUENCE 420 AA; 47448 MW; 370C84AlBF398D24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 AA.
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                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similar to BCS1-like (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24,
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01-JUN-2003 (TrEMBLrel.
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STRAIN=cv Columbia, MEDIATIO97, MEDIATE.2003487; Publed=106171997, MEDIATE.2003487; Publed=106171997, Eurin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Bugli C.Y., Kerchum K.A., Lee T.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon b.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Coppenhaver G.P., Preuss D., Miserman W.C., White O., Elsen J.A., "Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Langston Y., Rohlfing T.;
Langston G. G. elegans cosmid C34G6.";
The sequence of C. elegans to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                         Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                     44017 MW; 5CFD4FE172B63E75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.7%;
                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00499; P67PHOX. PRINTS; PR00452; SH3DOMAIN. ProDom; PD000066; SH3; 1. ProDom; PD003686; VHS; 1. SMART; SN00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDESNPHWWTGR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSS0002; SH3; 1.
PROSITE; PSS0330; UIM; 1.
PROSITE; PSS0179; VHS; 1.
SEQUENCE 397 AA; 44017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                               Pfam; PF00018; SH3; 1.
Pfam; PF02809; UIM; 1.
Pfam; PF00790; VHS; 1.
                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=Bristol N2;
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Best Local Similarity
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                                                                                                                                                                                           Waterston R.;
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SEQUENCE FROM N.A.
Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P., Chan M.C., Chang C.H., Dale J.M., Hayashizaki Y., Hanan V.W., Ishida J., Jones T., Kaminya A., Karlih-Neumann G., Kawai J., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sarou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, BT003105; AA0245371, -.
SEQUENCE 196 AA; 22564 MW, AE73517A9F41F181 CRC64;
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.

NCBI_TaxID=3702,
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Kim J.H., Kende H.;

"A novel class of transcription activators interacting with co-activators in Arabidogsis.";

Submitted (MAY-2002) to the BMBL/GenBank/DDBJ databases.

BMBL; AY102637; AAM52879.1;

SEQUENCE 380 AA; 42533 MW; AFFFF9791CCBE68D1 CRC64;
                                                                                                                                                                                                        Score 44; DB 10; Length 196; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.7%; Score 44; DB 10; Length 380; 58.3%; Pred. No. 54; Live 1; Mismatches 4; Indels
                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Prion-like-(q/n-rich)-domain-bearing protein 19, isoform
                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            380 AA.
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                        55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 58.3.,
Rest ... 7; Conservative
                                                                                                                                                                                                                                                                                               PHHOPSWYWGRG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 PHHQPSWYWGRG 148
                                                                                                                                                                                                                     Similarity 58.3 7; Conservative
                                                                                                                                                                                                                                                                  2 PDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription activator.
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Best Local S:
Matches 7,
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Q81712;
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Q8L8A7
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Gaps

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RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RA Lin X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

RI SEQUENCE FROM N.A.

RA M novel class of transcription activators interacting with putative co-activators in Arabidopsis.";

RT "A novel class of transcription activators interacting with putative RT "A novel class of transcription activators in Arabidopsis.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RT Co-activators in Arabidopsis.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

BR EMBL; AZ102636; AAM52878.1; -.

DR EMBL; AZ102636; AAM52878.1; -.

Query Match

Best Local Similarity 63.6%; Pred. No. 56;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy Z PDINPAWYTGR 12

Oy Z PDINPAWYTGR 12

DD 130 PHYQPAWYLGR 140

Search completed: August 12, 2004, 14:49:03
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Hinuma S, Habata Y,
Kitada C;
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therapeutic agent
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15-MAR-1996;
12-AUG-1996;
18-SEP-1996;
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06-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                   Rat type
Rat type
Rat cype
Rat CRH r
Peptide p
Rat type
Rat cxyto
Rat CKH r
Peptide p
Rat CKH r
Rat CYPE
Murine pi
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Prolactin
Rat CRH r
Rat PrRP-
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Rat oxyto
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Rat type
19P2 liga
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19P2 liga
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133.146 Million cell updates/sec
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                                                                                         August 12, 2004, 14:37:35 ; Search time 27.5872 Seconds
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Aay87504 I
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Aaw95174
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                            - protein search, using sw model
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AAB10359
AAG62528
ABU60841
AAW31389
AAB10360
AAG62529
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AAB90994
AAG62527
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ABU60840
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AAW95174
AAW95173
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AAB10355
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AAY49302
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Gapop 10.0 , Gapext 0.5
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genesequ200s:*
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genesequ2003as:*
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length: 2000000000
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Prol Rat Pept Pept Rat Rat Pept	Rat type Rat CRH z Peptide p Murine pi Rat type Rat type Rat type Rat cype Rat CRH z bbrrg31 p
	Aaw31386 Aab10357 Aab60839 Abu60839 Aaw91217 Aaw97225 Aab10354 Aab62523 Aab73370
AAB90993 AAG62524 AAE26400 ABU60826 ABU60837 AAB101385 AAB101385 AAG62525	AAW31386 AAB10357 ABU60839 AAW95172 AAW31383 AAW9725 AAW9725 AAW9725 AAB13370
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## ALIGNMENTS

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agent for dementia, depression, hyperkinetic syndrome, disturbance of consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperlipidaemia, hyperlipidaemia, hypercholesterolaemia, hypergyoclactinaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, rheumatoid arthritis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, infertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the G protein-coupled receptor protein. (Updated on 27-AuG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                           Murine pituitary-derived ligand polypeptide antigenic epitope.
                                                                                                                                                                                                  100.0%; Score 79; DB 2; Length 20; 100.0%; Pred. No. 4.3e-06;
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                                                                                                                                                                                                           100.0%; Pred. no.
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                                                                                                                                                                                                               Local Similarity 100.
es 13; Conservative
                                                                                                                                                                           Sequence 20 AA;
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                                                                                                                                                                                                    Query Match
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GPRIO; UHR-1; modulator; pitultary; central nervous system; pancreas; tissue; screen; therapeutic; binding; senile dementia; ligand; murine; Alzheimer's disease; Parkinson's disease; Huntington's disease; drug; Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone; secretion; diabetes; cancer; Theumatoid arthritis; epilepsy; vasopressor; gene therapy; transgenic animal; epitope.

Mus sp

WO9849295-A1.

05-NOV-1998

98WO-JP001923 27-APR-1998; 97JP-00109974. 28-APR-1997;

(TAKE ) TAKEDA CHEM IND LTD

Fukusumi S; Hinuma S,

WPI; 1999-009423/01.

The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated (PRR10 (human) or URR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor; to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, polypeptide ligand for orphan G protein coupled receptors - used for ating disorders of central nervous system, pituitary and pancreas, and Disclosure, Page 26; 206pp; English. for drug screening treating

The present sequence represents a rat type ligand fragment. It is used in the course of the invention. The specification describes an agent for modulating prolactin secretion which comprises a ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR) protein. The agents for promoting prolactin secretion can be used for treating or preventing

Claim 3; Page 154; 241pp; English.

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e.g. to treat semile dementia; Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; disabetes; schizophrenia; disorders of growth hormone secretion, cancer; rheumatoid arthritis, epilepsy and many others, also to improve postoperative mutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutein are used to study the function of the polypeptide-expressing genes, as models of disease, for drug screening and as source of cell lines. The ligand polypeptide DNA is used as a source of probes and primers; to identify related sequences; in receptor-binding assays; for production of Ab and antisera; in drug development; for gene therapy and to develop transgenic animals. Sequences AAW95174 represent antigenic epiotpes which can be used for the preparation of anti-ligand polypeptide antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat type ligand; modulation; prolactin secretion; g protein-coupled receptor; GPCR; hypowarianism; gonecyst cacogenesis; menopausal syndrome; euthyroid; hypometabolism; lactation; pitultary adenomatosis; brain tumour; emmeniopathy; autoimmune disease; prolactinoma; infertility; impotence; amenorrhea; galactorrhea; acromegaly; Chiari-Frommel syndrome; Argonz-del Castilo syndrome; Porbes-Albright syndrome; Iymphoma; Sheehan syndrome; dyszoospermia; contraceptive; placental function; choriocarcinoma; hydatid mole; irruption mole; abortion; unthrifty fetus; abnormal saccharometabolism; abnormal lipidmetabolism; oxytocia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of G protein-coupled receptor ligands - for modulating prolactin secretion or placental function, e.g. for treating menopausal syndrome, tumours, autoimmune disease or abnormal pregnancy.
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100.0%; Pred. No. 4.3e-06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat type ligand polypeptide fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW97234 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                      Sequence 20 AA;
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hypocvarianism, gonecyst cacogenesis, menopausal syndrome, euthyroid or hypometabolism. They can by used for promoting lactation in a domestic mammal and as an aphrodisiac. The agents for inhibiting prolactin secretion can be used for treating or preventing pituitary adenomatosis, brain tumour, emmeniopathy, autoimmune disease, prolactinoma, imporence, amenorthea, galactorrhea, acromegaly, Chiari-Frommel syndrome, Argonz-del Castilo syndrome, Porbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszospermia. The inhibitory agents can also be used as contraceptives. The agents for modulating placental function can be used for treating or preventing chriscarcinoma, hydatid mole, irruption mole, abortion, unthrifty feuts, abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides a monoclonal antibody which has a specific reaction with the part peptide of the C-terminal of 1992 ligand or its derivative. The antibodies can be used in diagnosis or to treat or prevent diseases associated with ahormality in the pituitary function regulatory mechanism (e.g. promotion of prolactin secretion), central nervous regulatory mechanism, and pancreatic function regulatory mechanism. The antibody-based immunoassay can also be applied in clarifying the physiological functions of the ligand and its derivative. Sequences AAY49290-302 represent peptide fragments of the 1992 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New monoclonal antibodies, useful in diagnosis, as drugs and in studying diseases related to ligand abnormality.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody, 19P2 ligand; diagnosis; prolactin secretion; pituitary; regulatory mechanism; central nervous system; pancreatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY49302 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19P2 ligand peptide fragment.
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                               Sequence 20 AA;
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Sequence 20 AA;

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                                                                                                                                                                                                                                                                                                Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cc caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. was an atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion
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                               Gaps
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 Length 20;
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                                                                                                                                                                                                                                                                       Rat oxytocin secretion promoting peptide SEQ ID NO: 21.
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100.0%; Pred. No. 4.3e-06;
ive 0; Mismatches 0;
 Score 79; DB 3; L. Pred. No. 4.3e-06; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB90994 standard; peptide; 20 AA.
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                                                                                                                                                                           AAB10358 standard; peptide; 20
   100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsumoto H, Kitada C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-452298/39.
Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp.
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently covalently active amino acid region (IV), which covalently bonds with amino/hydroxyl/thioi groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic control peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

Compatible and specificity as bonding to large molecules decreases for reduces the action of peptidases to increase length of activity (half littacellular uptake and interference with physiological processes.

Chabsonso to AABSO241 represent invention

Compatible activity the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                      Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl, maleimido group, amino, hydroxyl; thiol; hormone, growth factor, neurotransmitter.
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                                                                     Prolactin releasing peptide SEQ ID NO:168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 245; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Milner PG,
                                                                                                                                                                                                                                                                                                                                        99US-0134406P.
99US-0153406P.
99US-0159783P.
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                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                              (CONJ-) CONJUCHEM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 AA;
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10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                             Homo sapiens.
                                  22-JUN-2001
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                                                                                                                                                                                              Synthetic.
 AAB90994;
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Rat CRH releasing protein related peptide SEQ ID NO: 21.

(first entry)

24-AUG-2001

XEXEXEX

AAG62527;

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AAG62527 standard; peptide; 20

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                                                                                                                                                                                                                                                                                                                Use of G protein receptor ligand or peptide for controlling corticotropin releasing hormone secretion.
                                                                                                                                                                                                                                                                                                                                                                                     The present sequence describes a method of controlling the secretion of corticotrophin releasing hormone (CRH), involving the use of a G protein receptor Thisand. This can be used to control the secretion of CRH and is useful as an analgesic or for treating, preventing or ameliorating diseases associated with CRH secretion such as hyperaldosteronism, hypercortisolaemia, secondary or chronic hypoadrenocorticism, Addison's disease (including boredom, nauses, pigmentation, hypogonadism, hair loss, and hypotension), adrenal gland hypofunction and obesity. The present sequence is a peptide used in the exemplification of the
Rat; corticotrophin releasing hormone; CRH; G protein receptor ligand; analgesic; hyperaldosteronism; hypercortisolaemia; hypoadrenocorticism; Addison's disease; adrenal gland hyperfunction; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; wakefulness; sleep disorder; prolactin releasing peptide receptor; PrRP; GPRL0; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea; insomnia; idiopathic hypersomnia; psychogenic hypersomnia; selzure; anticonvulsant.
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100.0%; Pred. No. 4.3e-06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 70; 90pp; Japanese.
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                                                                                                                                                                                                                                                       Matsumoto H, Hinuma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE26403 standard; peptide; 20
                                                                                                                                                  L7-NOV-2000; 2000WO-JP008119.
                                                                                                                                                                                             26-SEP-2000; 2000JP-00297073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-2001; 2001US-00932161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
es 13; Conservative
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                                                                                        WO200135984-A1.
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                                                                                                                                                                              .8-NOV-1999;
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                                                                                                                    25-MAY-2001.
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                                                                                                                                                                                                                                                       Kitada C,
                                                           Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
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W09724436-A2
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06-APR-1998
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Matches
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AAW31388
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                                                                                                                                                The present invention relates to a method of screening for compounds for peromoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PrRP) receptor (GPRIO) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. PrRP receptor agonists may be used to treat common disorders which lead psychogenic hypersomnia. PrRP receptor antagonists are useful for picconding sleep and for treating insomnia such as adjustment sleep disorder and psychophysiologic insomnia. The present sequence is rat PrRP-31 C-terminal peptide, PrRP-20
                                                                    Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide production by gene recombination associated peptide #24.
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Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                                               Disclosure; Page 24; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU60840 standard; peptide; 20
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                                                      WPI; 2002-403931/43
                                Lin S;
 CIVELLI O.
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                                                                                                                                                                                                                                                                                                                     Sequence 20 AA;
            LIN S.
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                               Civelli O,
 CIVE/)
            (LINS/)
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This sequence represents a peptide fragment from a novel rat type ligand polypeptide corresponding to amino acid residues 33 to 53 of the sequence represented in AAW31383 and is used in an assay to monitor ligand binding to the G protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pannoratic function modulator. This ligand could have specific applications as a prophylactic or therapeutic agent for dementia, depression, hyperkinetic syndrome, disturbance of
                                                    The invention describes a method of producing a peptide comprising the excision of the N and C-terminals of a target peptide with enzymes or chemically through the attached cleavage sites repeated by ligation in a precursor protein. The method is for producing (low-molecular) peptide e.g. KiSS-1 peptide and GRR8 ligand for subsequent applications by the gene recombination technique through tandem repeats to provide a precursor protein with specific cleavage sites. With this method, peptide production can be carried out easily to provide large quantities of the required peptides. This is the amino acid sequence of a peptide associated with the peptide production method of the invention
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pituitary; central nervous system; pancreas; prophylactic;
therapeutic agent.
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Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
Disclosure, Page 65; 87pp; Japanese.
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96JP-00059419.
96JP-00211805.
96JP-00246573.
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(first entry)
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nes 13; Conservative
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15-MAR-1996;
12-AUG-1996;
18-SEP-1996;
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Gaps

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Length 21;

100.0%; Score 79; DB 3; I 100.0%; Pred. No. 4.5e-06; Mismatches

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Conservative

Similarity 13; Conserv

Query Match Best Local S Matches 13

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consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone secretory disease, hyper- and polyphagia, hyperprolactinaemia, hypercholesterolaemia, hyperprolactinaemia, diabetes, cancer, panoreatitis, renal disease, Turner's syndrome, neurosis, asthmantheumatoid arthitis, spinal injury, transient brain ischaemia, epilepsy, amylotrophic lateral sclerosis, acute myocardial infarction, lifertility, spinocerebellar degeneration, bone fracture, trauma, atopic dermatitis, osteoporosis and/or oligogalactia. Assays can also be developed to screen compounds which are capable of altering the binding activity of the ligand affecting activation of the g protein-coupled receptor protein. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat, oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; or caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat oxytocin secretion promoting peptide SEQ ID NO: 22.
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Best Local Similarity
                                                                                                                                                                     Sequence 21 AA;
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                                                                                                                                 Rat, corticotrophin releasing hormone, CRH, G protein receptor ligand, analgesic, hyperaldosteronism, hypercortisolaemia, hypoadrenocorticism, Addison's disease, adrenal gland hyperfunction, obesity.
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                                                                                                   CRH releasing protein related peptide SEQ ID NO: 22.
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             21
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26-SEP-2000; 2000JP-00297073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              releasing hormone secretion.
           AAG62528 standard; peptide;
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                                                                         (first entry)
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Best Local Similarity
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                                          AAG62528;
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COW;

This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of drugs for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, uterine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion

Sequence 21 AA;

promoter

Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.

Disclosure; Page 58; 72pp; Japanese.

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Fukusumi

Rattus sp.

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This sequence represents a peptide fragment from a novel rat type ligand corresponding to amino acid residues 33 to 54 of the sequence polypeptide corresponding to amino acid residues 33 to 54 of the sequence represented in AAA31383 and is used in an assay to monitor lagand binding to the the protein-coupled receptor protein. Pharmaceutical compositions containing this ligand may be used as a pituitary function modulator, a central nervous system modulator or a pancreatic function modulator. This containing this ligand modulator or a pancreatic function modulator. This control nervous system modulator or a pancreatic function modulator. This consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone consciousness, anxiety syndrome, schizophrenia, trauma, growth hormone consciousness, anxiety syndrome, schizophrenia, typercholacturaemia, diabetes, hypercholacterolacmia, hypercylveriddemia, hypercholacturaemia, diabetes, cancer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, concer, pancreatitis, renal disease, Turner's syndrome, neurosis, asthma, concern, any lotrophic lateral solerosis, acute myocardial infarction, infertility, splnocerbellar degeneration, bone fracture, trauma, atopic dermatitis, compounds which are capable of altering the binding activity of the lighdated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; oxytocin secretion promoter; G protein-coupled receptor protein; treatment; disease; pain; atonic bleeding; uterine recovery failure; cow; caesarean section; artificial fertilization; galactostasis; goat; pig; veterinary medicine; milk production.
                                                                                                                                                                                                                                                                                                                 peptide for G protein-coupled receptor - acts by modulating on in the central nervous system, pancreas and pituitary gland.
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                                                                                                                                                                          Hosoya M, Fujii R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat oxytocin secretion promoting peptide SEQ ID NO:
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                                                                                                                                                                               Kawamata Y,
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              95JP-00343371.
96JP-00059419.
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Best Local Similarity luv.
Local 3, Conservative
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                                                                                                                                  (TAKE ) TAKEDA CHEM IND
                                                                                                                                                                               Habata Y,
                                                                                                                                                                                                                                                 WPI; 1997-363672/33.
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                 28-DEC-1995;
15-MAR-1996;
12-AUG-1996;
18-SEP-1996;
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                                                                                                                                                                                 Hinuma
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                                                                                                                                                                                                       Kitada
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AAB10360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by gene recombination technique through tandem repeats to provide precursor protein with specific cleavage sites.
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                                            Peptide production by gene recombination associated peptide #25
                                                                                   Peptide production, low-molecular peptide, KiSS-1; GPR8 ligand, gene recombination.
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pituitary; central nervous system; pancreas; prophylactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat type G protein-coupled receptor ligand fragment 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 66; 87pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                    17-MAY-2001; 2001JP-00147341.
                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-129302/12.
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06-APR-1998
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  06-MAY-2003
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AAW31389;

RESULT 14 AAW31389

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Gaps

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0; Indels

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This invention describes a novel oxytocin secretion-regulating agent which contains a ligand peptide or its salt for the G protein-coupled receptor protein. It is useful in the form of furges for ameliorating, preventing and treating diseases relating to oxytocin secretion e.g. weak pains and atonic bleeding, before and after expulsion of placenta, therine recovery failure, caesarean section, stoppage of artificial fertilization or galactostasis and is also applicable in veterinary medicine for promoting milk production in cow, goat and pig. This sequence represents a rat peptide which acts as an oxytocin secretion
                                                                                                                                                                      Physiologically-active polypeptide recognized as ligand by G protein-coupled receptor protein, for promoting secretion of oxytocin, as drugs for diseases relating to oxytocin secretion and in veterinary medicine.
                                                                                                                                                                                                                                                             Disclosure; Page 59; 72pp; Japanese.
                                                                                       Kitada C, Hinuma S;
  25-DEC-1998; 98JP-00369585.
                                         (TAKE ) TAKEDA CHEM IND LID.
                                                                                                                              WPI; 2000-452298/39.
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Sequence 22 AA;

; 0 Query Match
100.0%; Score 79; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 13; Conservative 0; Mismatches 0; Indels

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Gaps

1 TPDINPAWYICRG 13 

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Search completed: August 12, 2004, 14:43:55 Job time : 27.7122 secs

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August 12, 2004, 14:49:10 ; Search time 22.9767 Seconds (without alignments) 177.617 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1292805 segs, 313927144 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                    US-09-700-643A-3_COPY_12_24
                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Seguence 43, Appl	Sequence 44, Appl	78	o	13,	σ,	13	equence 40	41	28	Seguence 38, Appl	82	84	8	OD.	18,	œ	15,	5	92	ω̈́	Sequence 268092,	Sequence 197, App	632	535, A	e 535	Sequence 574, App	169	74, A	Sequence 356, App
US-10-044-592-43	US-10-044-592-44	US-10-044-592-78	US-10-044-592-26	US-09-932-161-13	US-10-044-592-39	US-10-096-777-13	US-10-044-592-40	US-10-044-592-41	US-10-044-592-28	US-10-044-592-38	US-10-044-592-82	US-10-044-592-84	US-10-044-592-86	US-10-044-592-88	US-09-932-161-18	US-10-096-777-18	US-09-932-161-15		US-10-044-592-92	US-10-044-592-8	US-10-424-599-268092	US-10-301-822-197	US-10-369-493-6327	US-09-925-302-535	US-09-925-302-535	10-408	-10-369-493-16	10-225	US-10-374-780A-356
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93.7	93.7	93.7	93.7	93.7	93.7	93.7	93.7	93.7	93.7	93.7	93.7	93.7	93.7	93.7	86.1	86.1	86.1	86.1	86.1	72.2	62.0	62.0	58.2	57.0	57.0	57.0	56.3	55.7	55.7
74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	68	68	68	68	68	57	49	49	46	45	45	45	44.5	44	44
16	17	18	19	20	21	22	23			56								34	35	36	3.7	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Sequence 17, Application US/09932161
Sequence 17, Application US/09932161
Sequence 17, Application US/09932161
Sequence 17, Application US/09932161
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Civelli, Olivier
TITLE OF INVENTION: Screening and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep
TITLE OF INVENTION: Promoting Wakefulness and Sleep
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2000-04-28
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTHER FEASTER FastsEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 20
TYPE: PRT

CORGANISM: Rattus

US-09-932-161-17

DESCRIPTION OF PRESENT O
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CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ: ID NO 14
LENGTH: 31
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                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
                                                                                                                                                       TYPE: PRT CORGANISM: Rattus US-09-932-161-14
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; ORGANISM: Murine
US-10-044-592-4
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Publication No. US20030171270A1
Fublication No. US20030171270A1
Fublication No. US20030171270A1
FUBREAL INFORMATION:
APPLICANT: Civelli, Olivier
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: The Ling To Prolactin Releasing Peptide (PrRP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/10/096,777
CURRENT FILING DATE: 2002-03-12
FRIOR APPLICATION NUMBER: US/09/560,915
FRIOR APPLICATION NUMBER: US/09/560,915
FRIOR SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 20
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TITLE OF INVENTION: Polypeptides, their Production and Use FILE REFERENCE: 2463US2P

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 2002-01-10

PRIOR APPLICATION NUMBER: US (9/403639

PRIOR PILING DATE: 1992-55-10

PRIOR PILING DATE: 1998-01923

PRIOR PILING DATE: 1998-04-27

PRIOR PILING DATE: 1998-04-28

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 6

LENGTH: 20
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100.0%; Pred. No. 1.5e-05;
cive 0; Mismatches 0; Indels
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US-09-932-161-14
US-09-932-161-14
is Gequence 14, Application US/09932161
is GENERAL INFORMATION:
is APPLICANT: Civelli, Olivier
is APPLICANT: Lin, Steven
if TITLE OF INVENTION: Screening and Therapeutic Methods For
if TITLE OF INVENTION: Promoting Wakefulness and Sleep
is FILE REPRENCE: P-UC 4679
is CURRENT APPLICATION NUMBER: US/09/932,161
                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
LOCATION: (1)...(20)
COTHER INFORMATION: antigen
US-10-044-592-6
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Best Local Similarity
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; ORGANISM: Rattus
US-10-096-777-17
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                                                                                                                                                                                                                                                                                                                TYPE: PRT
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Sequence 4, Application US/10044592;
Publication No. US2020143152A1
GENERAL INFORMATION:
MAPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use
TITLE OF INVENTION: Polypeptides, their Production and Use
TITLE OF INVENTION: Polypeptides, their Production
PREBRICE: 2463U526;
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
FROM THE OF SEQ ID NOS: 96
SEG ID NO 4
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Sequence 5, Application US/10044592;
Publication No. US20020143152A1;
GENERAL INPORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use;
FILE REPRENCE: 2464082P
CURRENT FILING DATE: 2002-01-10
PRIOR PRILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1998-04-27
SPRIOR FILING DATE: 1998-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 31,
Length 31;
                                                      0; Indels
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100.0%; Score 79; DB 13;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 13; Conservative 0; Mismatches 0;
  100.0%; Score 79; DB 9; 1
100.0%; Pred. No. 2.3e-05;
                                                         0; Mismatches
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Gaps
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APPLICANT: Hinum, Shuji
APPLICANT: Hinum, Shoji
ITILE OF INVENTION: Polypetides, their Production and Use
FILE REPERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR PILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-25-10
PRIOR PILING DATE: 1997-04-28
NUMBER: OF SEQ ID NOS: 96
SOFTWARE:
SOFTWARE:
SOFTWARE:
SOFTWARE:
SEQ ID NOS: 96
LENGTH: 86
                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10044592;
Sequence 1, Application US/10044592;
Publication No. US2020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hinuma, Shuji
ITILE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION WUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US/99/403639
PRIOR FILING DATE: 1999-25-10
PRIOR PILING DATE: 1999-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 1
SEQ ID NO 1
  Best Local Similarity 100.0%; Score 79; DB 13; Length 70; Matches 13; Conservative 0; Mismattat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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; LOCATION: (1224)..(1243)
; OTHER INFORMATION: Bracket region depicted in FIG 39.
US-10-044-592-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 96, Application US/10044592; Publication No. US20020143152A1; GENERAL INFORMATION:
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                                                                                                                                                 1 TPDINPAWYTGRG 13
                                                                                                                                                                                                 33 TPDINPAWYTCRG 45
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ORGANISM: Murine
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US-10-044-592-96
US-10-044-592-90
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Sequence 14, Application US/10096777

Sequence 14, Application US/10096777

BUBILCALIN OF US20030171270A1

APPLICANT: Civelli, Olivier

APPLICANT: Lin, Steven

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Therapeutic Compositions Peptide (PrRP)

TITLE OF INVENTION: Therapeutic Compositions Peptide (PrRP)

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Therapeutic Compositions and Methods

TITLE OF INVENTION: Therapeutic Composition Releasing Peptide (PrRP)

FILE REFERENCE: P-02-03-12

PRIOR APPLICATION NUMBER: US/09/560,915

PRIOR APPLICATION NUMBER: US/09/560,915

PRIOR PILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PASSEQ for Windows Version 4.0

LENGTH: 31
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Fublication No. US20020143152A1

GENERAL INFORMATION:

APPLICANT: Humana, Shuji

APPLICANT: Humana, Shuji

APPLICANT: Humana, Shuji

APPLICANT: Humana, Shuji

TITLE OF INVENTION: Polypeptides, their Production and Use

FILE REPERENCE: 2463US2B;

CURRENT APPLICATION NUMBER: US/10/044,592

CURRENT FILING DATE: 1999-25-10

PRIOR FILING DATE: 1999-25-10

PRIOR FILING DATE: 1999-25-10

PRIOR APPLICATION NUMBER: PCT/JP98/01923

PRIOR FILING DATE: 1999-6-27

PRIOR APPLICATION NUMBER: JF 9-109974

PRIOR FILING DATE: 1997-04-28

NUMBER OF SEQ ID NOS: 96

SOFTWARE

SEQ ID NO 90

LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                       100.0%; Score 79; DB 13; Length 31; 100.0%; Pred. No. 2.3e-05; tive 0; Mismatches 0; Indels
     SEQ ID NO 5
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
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NAME/KEY: PEPTIDE
LOCATION: (1)..(31)
OTHER INFORMATION: antigen
                                                                                                                                                                                                                                                                                                                                                             1 TPDINPAWYTGRG 13
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Matches 13; Conservative
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CRGANISM: Rattus
US-10-096-777-14
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US-10-044-592-90
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US-10-044-592-5
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Publication No. US2020143152A1;
GENERAL INFORMATION:
APPLICANT: Hindma, Shuji
APPLICANT: Futusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION WIMBER: US 09/403639
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION WUMBER: UP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 42
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                     US-09-32-161-16
US-09-32-161-16
Sequence 16, Application US/09932161
Sequence 16, Application US/09932161
Setent No. US20020037533A1
GENERAL INFORMATION:
APPLICANT: Civelli, Olivier
APPLICANT: Civelli, Olivier
APPLICANT: Lin, Stevening and Therapeutic Methods For TITLE OF INVENTION: Promoting Wakefulness and Sleep
TITLE OF INVENTION: Exemening Makefulness and Sleep
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOSTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                   Score 74; DB 13; Length 19;
Pred. No. 8.8e-05;
0; Mismatches 1; Indels
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Pred. No. 9.2e-05;
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Pred. No. 9.2e-05;
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                                                                                                                                                                                                                             1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                     1 TPDINPAWYAGRG 13
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                                                                                                                                                                                12; Conservative
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TYPE: PRT
ORGANISM: Bos taurus
US-09-932-161-16
                                                                                                                                                             Best Local Similarity
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Best Local Similarity
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Best Local Similarity
; SEQ ID NO 27
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Bovine
US-10-044-592-27
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US-10-044-592-42
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US-10-044-592-42
                                                                                                                                      Query Match
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COTHER INFORMATION: insert fragment of pmGB3 as depicted in FIG 36 and 37.
US-10-044-592-94
                                                                    Gaps
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APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2453US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-26-40
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: DCT/JP98/01923
PRIOR APPLICATION NUMBER: DP 9109974
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APPLICANT: Fukusumi, Shoji
APPLICANT: Fukusumi, Shoji
TILE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION UNMER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1998-04-27
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
                         Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 79; DB 13; Length 91; 1 Similarity 100.0%; Pred. No. 6.4e-05; 13; Conservative 0; Mismatches 0; Indels
                                                               0; Indels
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                Query Match

100.0%; Score 79; DB 13;
Best Local Similarity 100.0%; Pred. No. 6.1e-05;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                        US-10-044-592-94
. Sequence 94. Application US/10044592
. Publication No. US2020143152A1
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(3)
OTHER INFORMATION: primer
NAME/KEY: misc_feature
LOCATION: (925)...(955)
OTHER INFORMATION: primer
NAME/KEY: misc_feature
                                                                                                         1 TPDINPAWYTGRG 13
                                                                                                                                                 33 TPDINPAWYTGRG 45
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SOFTWARE:
SEQ ID NO 94
LENGTH: 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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US-10-096-777-16
sequence 16, Application US/10096777
sequence 16, Application No. US20330171270A1
sequence 16, Publication No. US20330171270A1
sequence 17, Application No. US20330171270A1
sequence 17, Application No. US20330171270A1
string of INVENTION: Therapeutic Compositions and Methods
string Reperence: P-UC 3534
cURRENT APPLICATION NUMBER: US/10/096,777
scurrent PTILING DATE: 2002-03-12
sprior PTILING DATE: 2000-04-28
sprior FILING DATE: 2000-04-28
Gaps
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Pred. No. 9.2e-05;
0; Mismatches 1; Indels
1; Indels
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 92.3%;
Matches 12, Conservative
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                                                                     1 TPDINPAWYTGRG 13
   12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Bos taurus
US-10-096-777-16
      Matches
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42, Appl 43, Appl 79, Appl 22, Appl 39, Appl 39, Appl 40, Appl 143, App 143, App 123, Appl 143, Appl 17, Appl 340709,

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Sequence 35, Application US/10477712B
Sequence 35, Application US/10477712B
GENERAL INFORMATION:
TITLE OF INVERTION: A Method for Producing A Peptide
FILE REPERENCE: OXA-0213
CURRENT APPLICATION NUMBER: US/10/477,712B
CURRENT FILING DATE: 2003-11-14
PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 85
LENGTH: 20
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US-10-477-712B-84

Sequence 84, Application US/10477712B

Sequence 84, Application US/10477712B

SEQUENCE 84, Application US/10477712B

TITLE OF INVENTION: A Method for Producing A Peptide

FILE REFERENCE: OKA-0213

CURRENT APPLICATION NUMBER: US/10/477,712B

PRIOR APPLICATION NUMBER: US/10/477,712B

PRIOR FILING DATE: 2003-11-14

PRIOR FILING DATE: 2001-05-17

NUMBER OF SEQ ID NOS: 85
Query Match
100.0%; Score 79; DB 6; I
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 13; Conservative 0; Mismatches 0;
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          Query Match
Best Local Similarity
Matches 13; Conserv
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US-10-477-712B-35
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1: /cgn2 6/ptodata/2/paa/USO6 NEW COMB.pep:*

2: /cgn2 6/ptodata/2/paa/USO6 NEW COMB.pep:*

3: /cgn2 6/ptodata/2/paa/USO7 NEW COMB.pep:*

4: /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

5: /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

6: /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

7: /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

7: /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*
                                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-477-7128-84
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Maximum Match 100%
Listing first 45 summaries
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1 TPDINPAWYTGRG 13
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
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US-10-477-712B-32; Sequence 32, Application US/10477712B; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity 100.
Marches 13; Conservative
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Best Local Similarity
Matches 13; Conserv
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ORGANISM: Bovine
                                   ; ORGANISM: Human
US-10-477-712B-37
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ORGANISM: RAT
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100.0%; Score 79; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
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US-10-477-712B-37
is Sequence 37, Application US/10477712B
sequence 37, Application US/10477712B
sequence 37, Application US/10477712B
sequence 1 reference 1 reference 1 reference 2 reference 2 reference 2 reference 2 reference 3 referen
                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INTENTION: A Method for Producing A Peptide
CURRENT APPLICATION NUMBER: US/10/477,712B
CURRENT APPLICATION NUMBER: US/10/477,712B
CURRENT APPLICATION NUMBER: US 2003-11-14
PRIOR PRING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 85
LENGTH: 21
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US-10-477-712B-76

Sequence 76, Application US/10477712B

GENERAL INFORMATION:

APPLICANT: Takeda Chemical Industries, Ltd.,

TILE OF INVENTION: A Method for Producing A Peptide

FILE REFERENCE: OKA-0213

CURRENT APPLICATION NUMBER: US/10/477,712B

CURRENT FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: JP 2001-147341

NUMBER OF SEQ ID NOS: 85

SEQ ID NO 76
   1 TPDINPAWYTGRG 13
                                          TPDINPAWYTGRG 13
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Matches 13; Conserv
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; ORGANISM: Bovine
US-10-477-712B-76
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; ORGANISM: Rat
US-10-477-712B-36
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Sequence 21, Application US/10477712B

GENERAL INPORMATION:

GENERAL INPORMATION:

TITLE OF INVENTION: A Method for Producing A Peptide

FILE REPRENCE: OKA-0213

CURRENT APPLICATION NUMBER: US/10/477,712B

CURRENT FILING DATE: 2003-11-14

PRIOR APPLICATION NUMBER: JP 2001-147341

PRIOR APPLICATION NUMBER: JP 2001-147341

NUMBER OF SEQ ID NOS: 85

LENTH: 31
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TITLE OF INVENTION: A Method for Producing A Peptide
100.0%; Score 79; DB 6; 100.0%; Pred. No. 2.8e-06;
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100.0%; Pred. No. 3.9e-06;
iive 0; Mismatches 0;
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TYPE: PRT
ORGANISM: Bovine
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Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
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Sequence 34, Application US/10477712B

Sequence 34, Application US/10477712B

GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: A Method for Producing A Peptide
FILE REFERENCE: CKA-0213
CURRENT APPLICATION NUMBER: US/10/477,712B
CURRENT FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
NUMBER OF SEQ ID NOS: 85
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICAT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: A Method for Producing A Peptide
FILE REPERENCE: OXA-0213
CURRENT PELING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US/10/477,712B
PRIOR APPLICATION NUMBER: JP 2001-147341
PRIOR PEPLING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 85
FILE REFERENCE: OKA-0213
CURRENT APPLICATION NUMBER: US/10/477,712B
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: JP 2001-147341
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 32
LENGTH: 31
TYPE: PRT
ORGANISM: RAL
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-10-477-712B-33
Sequence 33, Application US/10477712B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TPDINPAWYTGRG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                        1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                                                                                           12 TPDINPAWYTGRG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-477-712B-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rat
                                                                                                                                                                                                   US-10-477-712B-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-477-712B-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 33
LENGTH: 32
TYPE: PRT
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12 TPDINPAWYTGRG 24

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; OTHER INFORMATION: the C-terminus of the polypeptide is amide (-CONH2) form US-10-069-228B-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 1.6e-05;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

Best Local Similarity 92.3%; Pred. No. 1.8e-05;
Matches 12; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-10-477-712B-25
US-10-477-712B-25
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TILE OF INVERNION: A Method for Producing A Peptide
FILE REFERENCE: OKA-0213
CURRENT APPLICATION NUMBER: US/10/477,712B
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: UP 2001-147341
PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-10-477-712B-29
US-10-477-712B-29
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; APPLICANT: Takeda Chemical Industries, Ltd.
; FILE REFERENCE: OKA-0213
; CURRENT APPLICATION UNMERE: US/10/477,712B
; CURRENT APPLICATION UNMERE: US/10/477,712B
; PRIOR APPLICATION NUMBER: JP 2001-147341
Sequence 15, Application US/10069228B

Sequence 15, Application US/10069228B

GENERAL INFORMATION:
APPLICANT: HINUMA, SHUJI
APPLICANT: HOSOYA, MASAKI
FILE PERENCE: 46342/57113
CURRENT APPLICATION SCREENING METHOD
FILE REFERENCE: 46342/57113
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: PCT/JP00/05639
PRIOR APPLICATION NUMBER: 9F11-236597
PRIOR APPLICATION NUMBER: JP1-236597
PRIOR FILING DATE: 1999-08-24
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 15
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.78;
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPDINPAWYTGRG 13
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                           Score 74; DB 6; Length 20;
Pred. No. 1.7e-05;
0; Mismatches 1; Indels
                                                                                                                                                             Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74; DB 6; Length 21;
Pred. No. 1.8e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-10-477-712B-82
US-10-477-712B-82
Sequence 82, Application US/10477712B
Sequence 82, Application US/10477712B
Sequence 82, Application US/10477712B
SEQUENCEMENT Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: A Method for Producing A Peptide
FILE REFRENCE: OKA-0213
CURRENT APPLICATION NUMBER: US/10/477,712B
CURRENT RILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: UP 2001-147341
PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 85
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-477-712B-23
US-10-477-712B-23
Sequence 23, Application US/10477712B
Sequence 23, Application US/10477712B
Sequence 23, Application US/10477712B
Sequence 23, Application US/10477712B
TITLE OF INVENTION: A Method for Producing A Peptide
FILE REPRENCE: OKA-0213
CURRENT APPLICATION NUMBER: US/10/477,712B
CURRENT FILING DATE: 2003-11-14
PRIOR PRILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 85
LENGTH: 21
                                                                                                                                                           93.7%;
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Best Local Similarity 92.3%;
Matches 12; Conservative C
PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 29
LENGTH: 20
                                                                                                                                                       Query Match
Best Local Similarity 92.3
Matches 12, Conservative
                                                                                                                                                                                                                                     1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                1 TPDINPAWYTGRG 13
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Bovine
US-10-477-712B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bovine
US-10-477-712B-82
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CRGANISM: Bovine
US-10-477-712B-23
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Search completed: August 12, 2004, 15:17:35 Job time : 11.7151 secs

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35, 36,

Sequence Sequence Sequence

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Query Match
100.0%; Score 79; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Suemaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENITON: METHOD OF PRODUCING A 19P2 LIGAND
WUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILNG DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGRNT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELEPRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 27
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US-09-105-678A-30
US-08-76-971-4
US-09-421-208-30
US-09-105-678A-34
US-08-776-971-8
US-08-776-971-9
US-09-421-208-35
US-09-156-915-16
US-09-156-915-16
US-09-156-915-16
US-09-105-678A-35
US-09-105-678A-35
US-09-105-678A-36
US-09-421-208-36
                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-09-105-678A-40
; Sequence 40, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-40
       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Appli
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                                                                                                                                August 12, 2004, 14:37:36; Search time 7.40698 Seconds (without alignments) 90.609 Million cell updates/sec
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Sequence 17,
Sequence 41,
Sequence 51,
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Sequence 42,
Sequence 52,
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Sequence 50,
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Sequence
Sequence
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1. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-776-971-50
US-09-421-50
US-09-421-50
US-09-105-678A-41
US-09-105-678A-41
US-09-105-678A-42
US-09-105-678A-42
US-09-105-678A-42
US-09-105-678A-8
US-09-105-678A-8
US-09-105-678A-8
US-09-105-678A-37
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US-09-105-678A-38
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US-08-776-971-124
US-08-776-971-137
                                                                                                                                                                                                                                                                                                                                        389414 segs, 51625971 residues
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                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                Scoring table:
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Maximum DB seq
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Query Match
Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-421-208-40
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                                                                                                                                                                                                                                    Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fusii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compactible
COMPUTER: IBM compactible
COMPUTER: IBM compactible
CORRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRINT APPLICATION DATA:
FILING DATE: 06-Feb-1997
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION: CUBATION:

APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: UP 8/59419
FILING DATE: 12-MAR-1996
APPLICATION NUMBER: UP 8/211805
FILING DATE: 12-MAR-1996
APPLICATION NUMBER: UP 8/211805
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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FRAGNENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-08-776-971-50
                                                                                                                                        Sequence 50, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                APPLICANT: Hinuma, Shuji
1 TPDINPAWYTGRG 13
                                                                                           RESULT 2
US-08-776-971-50
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Sequence 40.28pt cation US/0341108
Sequence 40.28pt cation US/0341108
Sequence 40.28pt cation US/0341108
Sequence 40.28pt cation US/0341108
APPLICANT: Suanga Masaco
APPLICANT: Standay Masaco
APPLICANT: Manhamiza Cosau
TITLE OF INVENTION: METHOD OF RECONCING A 19P2 LICAND
CONTRES: 130 Water Street
CONTRES: 27 UNN 199
FILLING DATE: 27 UNN 199
FILLING THE STREET STREE
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1 TPDINPAWYTGRG 13

RESULT 3

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Gaps
                           Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL TO SERVICE OF THE PARTICION ON THE PARTICION ON SERVICE OF THE PARTICION ON SERVICE OF THE PARTICION OF THE PARTICION
                                                                                                                                                                                                                                                                                                                                                  COMPTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FeatSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: «UNKNOWIN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/34331
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 12-M2-196
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-M2-196
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INPORMATION:
NAME: COALIN, David G.
REGISTRATION NUMBER: 27,026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
    TOPOLOGY: linear
    MOLECULE TYPE: protein
    FRAGMENT TYPE: internal
    SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-08-776-971-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 47176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                           STREET: 130 Water Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 51: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                                                             STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-421-208-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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                                                                                                                                    Gaps
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| Patent No. 6103892
| GENESAL INVORMATION:
| APPLICANT: Suenaga, Masato
| APPLICANT: Moriya, Takeo
| APPLICANT: Moriya, Takeo
| APPLICANT: Moriya, Takeo
| APPLICANT: Moriya, Takeo
| APPLICANT: Mishimura Osamu
| TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
| NUMBER OF SEQUENCES: 52
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
| STREET: 130 Water Street
| CITY: BOSCON
| STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 21;
                                                                  Length 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2e-06;
                                                           Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 79; DB 3; 100.0%; Pred. No. 1.2e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conlin, David G.
REGISTRATION UNBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 51, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 amino acids
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                                                                                                                                                                                                   1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                    1 TPDINPAWYTGRG 13
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-105-678A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-105-678A-41
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   US-09-560-915-17
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Kawamata, Yuji
Hosoya, Masaki
Hosoya, Masaki
Fujii, Ryo
Fujii, Ryo
Fujia, Ryoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                Length 22;
                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT IFFE: DESCRICE
CONTUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASEEEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION DATA:
APPLICATION DATA:
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 7/343371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: UP 8/59419
FILING DATE: 15-MAR-1996
FILING DATE: 15-MAR-1996
FILING DATE: 15-MAR-1996
FILING DATE: 15-MAR-1996
                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 79; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 52, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 12-AUG-1996
                 REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 4846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide US-09-105-678A-42
                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-776-971-52
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1.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Toko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: DIXE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
130 Water Street
                                                                                                                                                                                                CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/421,208

FILING DATE:

FILING DATE: 26-JUN-1998

APPLICATION NUMBER: US 09/105,678

FILING DATE: 26-JUN-1997

ATTONEY/AGENT INFORMATION:

NAME: COLLIN, David G.

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

REGISTRATION NUMBER: 27,026

RELECOMMUNICATION INFORMATION:

TELEBEROE (50-523-3400)

TELEBERAS: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA::
APPLICATION NUMBER: JP 172118/1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

100.0%; Score 79;

Best Local Similarity 100.0%; Pred. No.

Matches 13; Conservative 0; Mismatch
                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 42, Application US/09105678A Patent No. 6103882
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 W
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
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SEQUENCE CHARACTERISTICS

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                                        ; Secondary Application US/09105678A
; Parent No. 6103882
; GENERAL INFORMATION:
APPLICANT: Moriya, Takeo
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
CORRESPONDENCE S: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: EN PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INPORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELEBCOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELBEAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 TPDINPAWYTGRG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
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US-09-105-678A-37
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Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42, Application US/09421208

Patent No. 6258541

GENERAL INFORMATION:
APPLICANT: Suenaga, Masaro
APPLICANT: Takeo
APPLICANT: Takeo
APPLICANT: Mishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CUTY: Boston
STATE: MA
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                             Length 22
                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421,208
FILING DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-UN-1998
FILING DATE: 27-UN-1997
ATTONEY/AGENT INPORMATION:
NUMBER: APPLICATION NUMBER: US 09/105,678
FILING DATE: 27-UN-1997
ATTONEY/AGENT INPORMATION:
                                                                                                                                                                           Query Match
100.0%; Score 79; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 13; Conservative 0; Mismatches 0;
                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-08-776-971-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: COLLIN, David G.
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TPDINPAWYTGRG 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-421-208-42
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Gaps
                                                                KILGIA, Chieko
TITLE OF INVENTION: DOLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.
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Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Tanaka, Yoko
APPLICANT: Tanaka, Yoko
APPLICANT: Nablimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                COMPUTEY: USA

COMPUTEY: USA

COMPUTER: Diskette

COMPUTER: Diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B

FILING DATE: 06-Feb-1997

CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
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100.0%; Pred. No. 1.8e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 3/4331
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/216573
FILING DATE: 18-SEP-1996
ATTONNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGWENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFRAX: 617-523-6440
                                                    Fukusumi, Shoji
         Hosoya, Masaki
Fujii, Ryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 13; Conservative
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Fatent No. 6197830
GENERAL INFORMATION:
APPLICANT: Stricker-Kongra, Alain
APPLICANT: Gu, Wei
TITLE OF INVENTION: GPRIO AS A TARGET FOR IDENTIFYING WEIGHT MODULATING COMPOUNDS
FILE REPRENCE: 07344/102001
CURRENT APPLICANTON NUMBER: US/09/172,353
CURRENT PILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 4
LENGTH: 31
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100.0%; Score 79; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 31;
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                                                                                                 O'STAMARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION NUMBER: UP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGRAT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-523-3400
TELEFAX: 617-523-3400
TELEFAX: 617-523-3400
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 79; DB 3; L 100.0%; Pred. No. 1.8e-06; vative 0; Mismatches 0;
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 47, Application US/08776971B Patent No. 6228984 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 TPDINPAWYTGRG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPDINPAWYTGRG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TPDINPAWYTGRG 13
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
GORGANISM: Mus musculus
US-09-172-353-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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US-08-776-971-47
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US-09-172-353-4
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: LEW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/421,208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 27-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: CONION, DAVIG
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 27,026
REGISTRATION NUMBER: 37,026
REDEPHONE: 617-523-5440
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-8
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Search completed: August 12, 2004, 14:52:14 Job time : 8.40698 secs

1 TPDINPAWYTGRG 13 

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